



# Full wwPDB EM Validation Report (i)

Feb 24, 2024 – 01:07 PM EST

PDB ID : 7KZQ  
EMDB ID : EMD-23086  
Title : Structure of the human Fanconi anaemia Core-ID complex  
Authors : Wang, S.L.; Pavletich, N.P.  
Deposited on : 2020-12-10  
Resolution : 4.30 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at  
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references \(i\)](#)) were used in the production of this report:

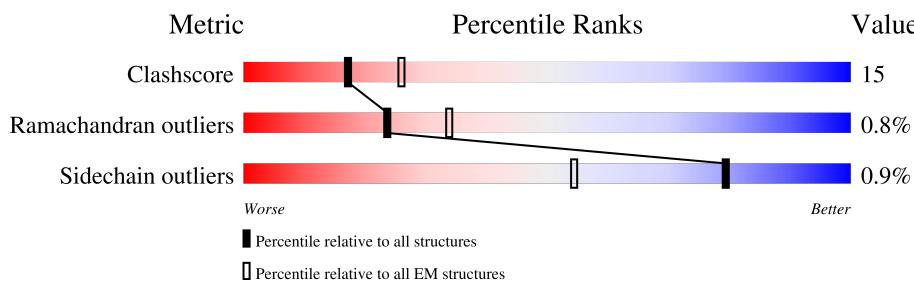
EMDB validation analysis : 0.0.1.dev70  
MolProbit : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
**ELECTRON MICROSCOPY**

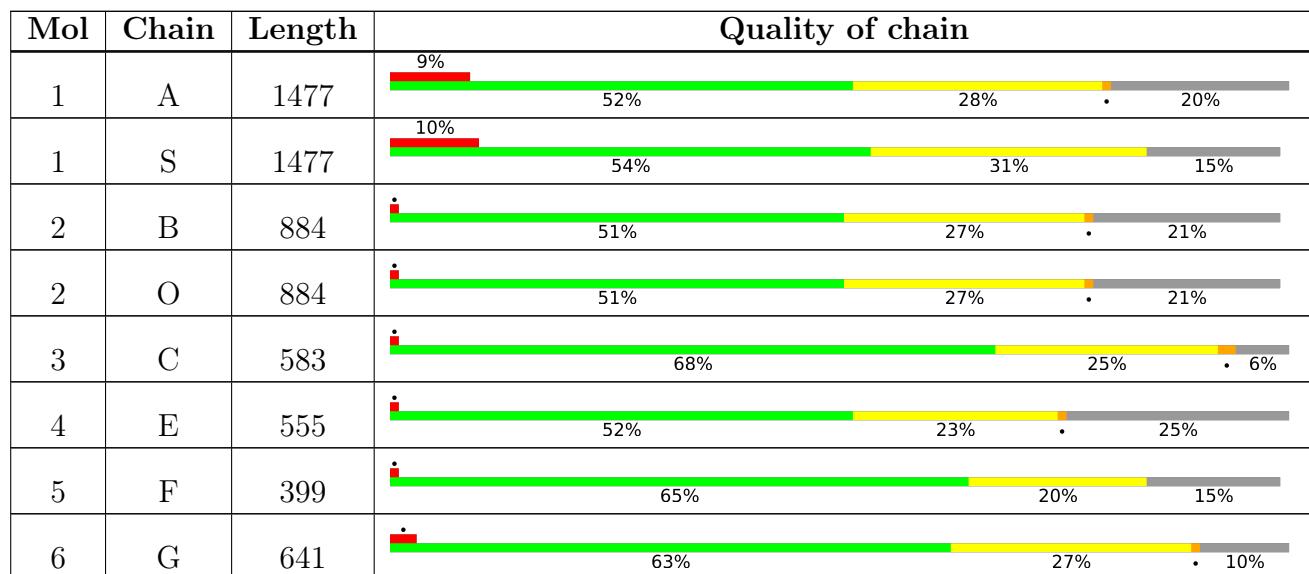
The reported resolution of this entry is 4.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.



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Mol	Chain	Length	Quality of chain			
6	H	641	61%	24%	15%	
7	L	394	72%	21%	6%	
7	M	394	65%	27%	6%	
8	P	906	50%	29%	17%	
8	Q	906	55%	27%	17%	
9	W	39	13%	56%	41%	
10	U	1328	55%	33%	12%	
11	V	1451	14%	49%	30%	21%

## 2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 172709 atoms, of which 87163 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Fanconi anemia group A protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	1186	18889	6001	9487	1650	1692	59	0	0
1	S	1250	19961	6345	10028	1747	1780	61	0	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1456	ALA	-	expression tag	UNP O15360
A	1457	ALA	-	expression tag	UNP O15360
A	1458	ALA	-	expression tag	UNP O15360
A	1459	LYS	-	expression tag	UNP O15360
A	1460	LEU	-	expression tag	UNP O15360
A	1461	VAL	-	expression tag	UNP O15360
A	1462	ASP	-	expression tag	UNP O15360
A	1463	GLU	-	expression tag	UNP O15360
A	1464	ASP	-	expression tag	UNP O15360
A	1465	LEU	-	expression tag	UNP O15360
A	1466	TYR	-	expression tag	UNP O15360
A	1467	PHE	-	expression tag	UNP O15360
A	1468	GLN	-	expression tag	UNP O15360
A	1469	SER	-	expression tag	UNP O15360
A	1470	ASP	-	expression tag	UNP O15360
A	1471	TYR	-	expression tag	UNP O15360
A	1472	LYS	-	expression tag	UNP O15360
A	1473	ASP	-	expression tag	UNP O15360
A	1474	ASP	-	expression tag	UNP O15360
A	1475	ASP	-	expression tag	UNP O15360
A	1476	ASP	-	expression tag	UNP O15360
A	1477	LYS	-	expression tag	UNP O15360
S	1456	ALA	-	expression tag	UNP O15360
S	1457	ALA	-	expression tag	UNP O15360
S	1458	ALA	-	expression tag	UNP O15360
S	1459	LYS	-	expression tag	UNP O15360

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Chain	Residue	Modelled	Actual	Comment	Reference
S	1460	LEU	-	expression tag	UNP O15360
S	1461	VAL	-	expression tag	UNP O15360
S	1462	ASP	-	expression tag	UNP O15360
S	1463	GLU	-	expression tag	UNP O15360
S	1464	ASP	-	expression tag	UNP O15360
S	1465	LEU	-	expression tag	UNP O15360
S	1466	TYR	-	expression tag	UNP O15360
S	1467	PHE	-	expression tag	UNP O15360
S	1468	GLN	-	expression tag	UNP O15360
S	1469	SER	-	expression tag	UNP O15360
S	1470	ASP	-	expression tag	UNP O15360
S	1471	TYR	-	expression tag	UNP O15360
S	1472	LYS	-	expression tag	UNP O15360
S	1473	ASP	-	expression tag	UNP O15360
S	1474	ASP	-	expression tag	UNP O15360
S	1475	ASP	-	expression tag	UNP O15360
S	1476	ASP	-	expression tag	UNP O15360
S	1477	LYS	-	expression tag	UNP O15360

- Molecule 2 is a protein called Fanconi anemia group B protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	701	Total	C	H	N	O	S	0	0
			11395	3619	5790	934	1013	39		
2	O	699	Total	C	H	N	O	S	0	0
			11353	3622	5759	926	1010	36		

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-24	MET	-	initiating methionine	UNP Q8NB91
B	-23	ASP	-	expression tag	UNP Q8NB91
B	-22	TYR	-	expression tag	UNP Q8NB91
B	-21	LYS	-	expression tag	UNP Q8NB91
B	-20	ASP	-	expression tag	UNP Q8NB91
B	-19	ASP	-	expression tag	UNP Q8NB91
B	-18	ASP	-	expression tag	UNP Q8NB91
B	-17	ASP	-	expression tag	UNP Q8NB91
B	-16	LYS	-	expression tag	UNP Q8NB91
B	-15	GLU	-	expression tag	UNP Q8NB91
B	-14	ASN	-	expression tag	UNP Q8NB91
B	-13	LEU	-	expression tag	UNP Q8NB91

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	TYR	-	expression tag	UNP Q8NB91
B	-11	PHE	-	expression tag	UNP Q8NB91
B	-10	GLN	-	expression tag	UNP Q8NB91
B	-9	GLY	-	expression tag	UNP Q8NB91
B	-8	GLY	-	expression tag	UNP Q8NB91
B	-7	GLY	-	expression tag	UNP Q8NB91
B	-6	ARG	-	expression tag	UNP Q8NB91
B	-5	LYS	-	expression tag	UNP Q8NB91
B	-4	LEU	-	expression tag	UNP Q8NB91
B	-3	GLY	-	expression tag	UNP Q8NB91
B	-2	THR	-	expression tag	UNP Q8NB91
B	-1	GLY	-	expression tag	UNP Q8NB91
B	0	SER	-	expression tag	UNP Q8NB91
O	-24	MET	-	initiating methionine	UNP Q8NB91
O	-23	ASP	-	expression tag	UNP Q8NB91
O	-22	TYR	-	expression tag	UNP Q8NB91
O	-21	LYS	-	expression tag	UNP Q8NB91
O	-20	ASP	-	expression tag	UNP Q8NB91
O	-19	ASP	-	expression tag	UNP Q8NB91
O	-18	ASP	-	expression tag	UNP Q8NB91
O	-17	ASP	-	expression tag	UNP Q8NB91
O	-16	LYS	-	expression tag	UNP Q8NB91
O	-15	GLU	-	expression tag	UNP Q8NB91
O	-14	ASN	-	expression tag	UNP Q8NB91
O	-13	LEU	-	expression tag	UNP Q8NB91
O	-12	TYR	-	expression tag	UNP Q8NB91
O	-11	PHE	-	expression tag	UNP Q8NB91
O	-10	GLN	-	expression tag	UNP Q8NB91
O	-9	GLY	-	expression tag	UNP Q8NB91
O	-8	GLY	-	expression tag	UNP Q8NB91
O	-7	GLY	-	expression tag	UNP Q8NB91
O	-6	ARG	-	expression tag	UNP Q8NB91
O	-5	LYS	-	expression tag	UNP Q8NB91
O	-4	LEU	-	expression tag	UNP Q8NB91
O	-3	GLY	-	expression tag	UNP Q8NB91
O	-2	THR	-	expression tag	UNP Q8NB91
O	-1	GLY	-	expression tag	UNP Q8NB91
O	0	SER	-	expression tag	UNP Q8NB91

- Molecule 3 is a protein called Fanconi anemia group C protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	C	550	8838	2826	4442	749	791	30	0	0

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-24	MET	-	initiating methionine	UNP Q00597
C	-23	ASP	-	expression tag	UNP Q00597
C	-22	TYR	-	expression tag	UNP Q00597
C	-21	LYS	-	expression tag	UNP Q00597
C	-20	ASP	-	expression tag	UNP Q00597
C	-19	ASP	-	expression tag	UNP Q00597
C	-18	ASP	-	expression tag	UNP Q00597
C	-17	ASP	-	expression tag	UNP Q00597
C	-16	LYS	-	expression tag	UNP Q00597
C	-15	GLU	-	expression tag	UNP Q00597
C	-14	ASN	-	expression tag	UNP Q00597
C	-13	LEU	-	expression tag	UNP Q00597
C	-12	TYR	-	expression tag	UNP Q00597
C	-11	PHE	-	expression tag	UNP Q00597
C	-10	GLN	-	expression tag	UNP Q00597
C	-9	GLY	-	expression tag	UNP Q00597
C	-8	GLY	-	expression tag	UNP Q00597
C	-7	GLY	-	expression tag	UNP Q00597
C	-6	ARG	-	expression tag	UNP Q00597
C	-5	LYS	-	expression tag	UNP Q00597
C	-4	LEU	-	expression tag	UNP Q00597
C	-3	GLY	-	expression tag	UNP Q00597
C	-2	THR	-	expression tag	UNP Q00597
C	-1	GLY	-	expression tag	UNP Q00597
C	0	SER	-	expression tag	UNP Q00597

- Molecule 4 is a protein called Fanconi anemia group E protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	E	419	6614	2048	3390	560	592	24	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-18	MET	-	initiating methionine	UNP Q9HB96
E	-17	ASP	-	expression tag	UNP Q9HB96

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-16	TYR	-	expression tag	UNP Q9HB96
E	-15	LYS	-	expression tag	UNP Q9HB96
E	-14	ASP	-	expression tag	UNP Q9HB96
E	-13	ASP	-	expression tag	UNP Q9HB96
E	-12	ASP	-	expression tag	UNP Q9HB96
E	-11	ASP	-	expression tag	UNP Q9HB96
E	-10	LYS	-	expression tag	UNP Q9HB96
E	-9	GLU	-	expression tag	UNP Q9HB96
E	-8	ASN	-	expression tag	UNP Q9HB96
E	-7	LEU	-	expression tag	UNP Q9HB96
E	-6	TYR	-	expression tag	UNP Q9HB96
E	-5	PHE	-	expression tag	UNP Q9HB96
E	-4	GLN	-	expression tag	UNP Q9HB96
E	-3	GLY	-	expression tag	UNP Q9HB96
E	-2	GLY	-	expression tag	UNP Q9HB96
E	-1	GLY	-	expression tag	UNP Q9HB96
E	0	ARG	-	expression tag	UNP Q9HB96

- Molecule 5 is a protein called Fanconi anemia group F protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	340	Total	C	H	N	O	S	0	0
			5466	1730	2740	506	483	7		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-24	MET	-	initiating methionine	UNP Q9NPI8
F	-23	ASP	-	expression tag	UNP Q9NPI8
F	-22	TYR	-	expression tag	UNP Q9NPI8
F	-21	LYS	-	expression tag	UNP Q9NPI8
F	-20	ASP	-	expression tag	UNP Q9NPI8
F	-19	ASP	-	expression tag	UNP Q9NPI8
F	-18	ASP	-	expression tag	UNP Q9NPI8
F	-17	ASP	-	expression tag	UNP Q9NPI8
F	-16	LYS	-	expression tag	UNP Q9NPI8
F	-15	GLU	-	expression tag	UNP Q9NPI8
F	-14	ASN	-	expression tag	UNP Q9NPI8
F	-13	LEU	-	expression tag	UNP Q9NPI8
F	-12	TYR	-	expression tag	UNP Q9NPI8
F	-11	PHE	-	expression tag	UNP Q9NPI8
F	-10	GLN	-	expression tag	UNP Q9NPI8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-9	GLY	-	expression tag	UNP Q9NPI8
F	-8	GLY	-	expression tag	UNP Q9NPI8
F	-7	GLY	-	expression tag	UNP Q9NPI8
F	-6	ARG	-	expression tag	UNP Q9NPI8
F	-5	LYS	-	expression tag	UNP Q9NPI8
F	-4	LEU	-	expression tag	UNP Q9NPI8
F	-3	GLY	-	expression tag	UNP Q9NPI8
F	-2	THR	-	expression tag	UNP Q9NPI8
F	-1	GLY	-	expression tag	UNP Q9NPI8
F	0	SER	-	expression tag	UNP Q9NPI8

- Molecule 6 is a protein called Fanconi anemia group G protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	G	577	Total	C	H	N	O	S	0	0
			9020	2843	4537	778	844	18		
6	H	544	Total	C	H	N	O	S	0	0
			8504	2676	4288	734	790	16		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-18	MET	-	initiating methionine	UNP O15287
G	-17	ASP	-	expression tag	UNP O15287
G	-16	TYR	-	expression tag	UNP O15287
G	-15	LYS	-	expression tag	UNP O15287
G	-14	ASP	-	expression tag	UNP O15287
G	-13	ASP	-	expression tag	UNP O15287
G	-12	ASP	-	expression tag	UNP O15287
G	-11	ASP	-	expression tag	UNP O15287
G	-10	LYS	-	expression tag	UNP O15287
G	-9	GLU	-	expression tag	UNP O15287
G	-8	ASN	-	expression tag	UNP O15287
G	-7	LEU	-	expression tag	UNP O15287
G	-6	TYR	-	expression tag	UNP O15287
G	-5	PHE	-	expression tag	UNP O15287
G	-4	GLN	-	expression tag	UNP O15287
G	-3	GLY	-	expression tag	UNP O15287
G	-2	GLY	-	expression tag	UNP O15287
G	-1	GLY	-	expression tag	UNP O15287
G	0	ARG	-	expression tag	UNP O15287
H	-18	MET	-	initiating methionine	UNP O15287

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-17	ASP	-	expression tag	UNP O15287
H	-16	TYR	-	expression tag	UNP O15287
H	-15	LYS	-	expression tag	UNP O15287
H	-14	ASP	-	expression tag	UNP O15287
H	-13	ASP	-	expression tag	UNP O15287
H	-12	ASP	-	expression tag	UNP O15287
H	-11	ASP	-	expression tag	UNP O15287
H	-10	LYS	-	expression tag	UNP O15287
H	-9	GLU	-	expression tag	UNP O15287
H	-8	ASN	-	expression tag	UNP O15287
H	-7	LEU	-	expression tag	UNP O15287
H	-6	TYR	-	expression tag	UNP O15287
H	-5	PHE	-	expression tag	UNP O15287
H	-4	GLN	-	expression tag	UNP O15287
H	-3	GLY	-	expression tag	UNP O15287
H	-2	GLY	-	expression tag	UNP O15287
H	-1	GLY	-	expression tag	UNP O15287
H	0	ARG	-	expression tag	UNP O15287

- Molecule 7 is a protein called E3 ubiquitin-protein ligase FANCL.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	L	370	Total	C	H	N	O	S	0	0
			5951	1914	2977	496	542	22		
7	M	370	Total	C	H	N	O	S	0	0
			5951	1914	2977	496	542	22		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-18	MET	-	initiating methionine	UNP Q9NW38
L	-17	ASP	-	expression tag	UNP Q9NW38
L	-16	TYR	-	expression tag	UNP Q9NW38
L	-15	LYS	-	expression tag	UNP Q9NW38
L	-14	ASP	-	expression tag	UNP Q9NW38
L	-13	ASP	-	expression tag	UNP Q9NW38
L	-12	ASP	-	expression tag	UNP Q9NW38
L	-11	ASP	-	expression tag	UNP Q9NW38
L	-10	LYS	-	expression tag	UNP Q9NW38
L	-9	GLU	-	expression tag	UNP Q9NW38
L	-8	ASN	-	expression tag	UNP Q9NW38
L	-7	LEU	-	expression tag	UNP Q9NW38

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-6	TYR	-	expression tag	UNP Q9NW38
L	-5	PHE	-	expression tag	UNP Q9NW38
L	-4	GLN	-	expression tag	UNP Q9NW38
L	-3	GLY	-	expression tag	UNP Q9NW38
L	-2	GLY	-	expression tag	UNP Q9NW38
L	-1	GLY	-	expression tag	UNP Q9NW38
L	0	ARG	-	expression tag	UNP Q9NW38
M	-18	MET	-	initiating methionine	UNP Q9NW38
M	-17	ASP	-	expression tag	UNP Q9NW38
M	-16	TYR	-	expression tag	UNP Q9NW38
M	-15	LYS	-	expression tag	UNP Q9NW38
M	-14	ASP	-	expression tag	UNP Q9NW38
M	-13	ASP	-	expression tag	UNP Q9NW38
M	-12	ASP	-	expression tag	UNP Q9NW38
M	-11	ASP	-	expression tag	UNP Q9NW38
M	-10	LYS	-	expression tag	UNP Q9NW38
M	-9	GLU	-	expression tag	UNP Q9NW38
M	-8	ASN	-	expression tag	UNP Q9NW38
M	-7	LEU	-	expression tag	UNP Q9NW38
M	-6	TYR	-	expression tag	UNP Q9NW38
M	-5	PHE	-	expression tag	UNP Q9NW38
M	-4	GLN	-	expression tag	UNP Q9NW38
M	-3	GLY	-	expression tag	UNP Q9NW38
M	-2	GLY	-	expression tag	UNP Q9NW38
M	-1	GLY	-	expression tag	UNP Q9NW38
M	0	ARG	-	expression tag	UNP Q9NW38

- Molecule 8 is a protein called Fanconi anemia core complex-associated protein 100.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	P	748	Total	C	H	N	O	S	0	0
			11279	3520	5681	972	1058	48		
8	Q	754	Total	C	H	N	O	S	0	0
			11355	3548	5724	978	1058	47		

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	-24	MET	-	initiating methionine	UNP Q0VG06
P	-23	ASP	-	expression tag	UNP Q0VG06
P	-22	TYR	-	expression tag	UNP Q0VG06
P	-21	LYS	-	expression tag	UNP Q0VG06

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-20	ASP	-	expression tag	UNP Q0VG06
P	-19	HIS	-	expression tag	UNP Q0VG06
P	-18	ASP	-	expression tag	UNP Q0VG06
P	-17	GLY	-	expression tag	UNP Q0VG06
P	-16	ASP	-	expression tag	UNP Q0VG06
P	-15	TYR	-	expression tag	UNP Q0VG06
P	-14	LYS	-	expression tag	UNP Q0VG06
P	-13	ASP	-	expression tag	UNP Q0VG06
P	-12	HIS	-	expression tag	UNP Q0VG06
P	-11	ASP	-	expression tag	UNP Q0VG06
P	-10	ILE	-	expression tag	UNP Q0VG06
P	-9	ASP	-	expression tag	UNP Q0VG06
P	-8	TYR	-	expression tag	UNP Q0VG06
P	-7	LYS	-	expression tag	UNP Q0VG06
P	-6	ASP	-	expression tag	UNP Q0VG06
P	-5	ASP	-	expression tag	UNP Q0VG06
P	-4	ASP	-	expression tag	UNP Q0VG06
P	-3	ASP	-	expression tag	UNP Q0VG06
P	-2	LYS	-	expression tag	UNP Q0VG06
P	-1	GLY	-	expression tag	UNP Q0VG06
P	0	SER	-	expression tag	UNP Q0VG06
Q	-24	MET	-	initiating methionine	UNP Q0VG06
Q	-23	ASP	-	expression tag	UNP Q0VG06
Q	-22	TYR	-	expression tag	UNP Q0VG06
Q	-21	LYS	-	expression tag	UNP Q0VG06
Q	-20	ASP	-	expression tag	UNP Q0VG06
Q	-19	HIS	-	expression tag	UNP Q0VG06
Q	-18	ASP	-	expression tag	UNP Q0VG06
Q	-17	GLY	-	expression tag	UNP Q0VG06
Q	-16	ASP	-	expression tag	UNP Q0VG06
Q	-15	TYR	-	expression tag	UNP Q0VG06
Q	-14	LYS	-	expression tag	UNP Q0VG06
Q	-13	ASP	-	expression tag	UNP Q0VG06
Q	-12	HIS	-	expression tag	UNP Q0VG06
Q	-11	ASP	-	expression tag	UNP Q0VG06
Q	-10	ILE	-	expression tag	UNP Q0VG06
Q	-9	ASP	-	expression tag	UNP Q0VG06
Q	-8	TYR	-	expression tag	UNP Q0VG06
Q	-7	LYS	-	expression tag	UNP Q0VG06
Q	-6	ASP	-	expression tag	UNP Q0VG06
Q	-5	ASP	-	expression tag	UNP Q0VG06
Q	-4	ASP	-	expression tag	UNP Q0VG06

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-3	ASP	-	expression tag	UNP Q0VG06
Q	-2	LYS	-	expression tag	UNP Q0VG06
Q	-1	GLY	-	expression tag	UNP Q0VG06
Q	0	SER	-	expression tag	UNP Q0VG06

- Molecule 9 is a protein called Fanconi anemia core complex-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	39	Total	C	H	N	O	0	0
			513	179	242	42	50		

- Molecule 10 is a protein called Fanconi anemia, complementation group I.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	U	1168	Total	C	H	N	O	S	0
			18882	5933	9626	1549	1720	54	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	877	LEU	ILE	conflict	UNP B7ZMF2
U	1235	VAL	ALA	conflict	UNP B7ZMF2
U	1274	SER	ASN	conflict	UNP B7ZMF2

- Molecule 11 is a protein called Fanconi anemia group D2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	V	1153	Total	C	H	N	O	S	0
			18733	5970	9475	1527	1709	52	

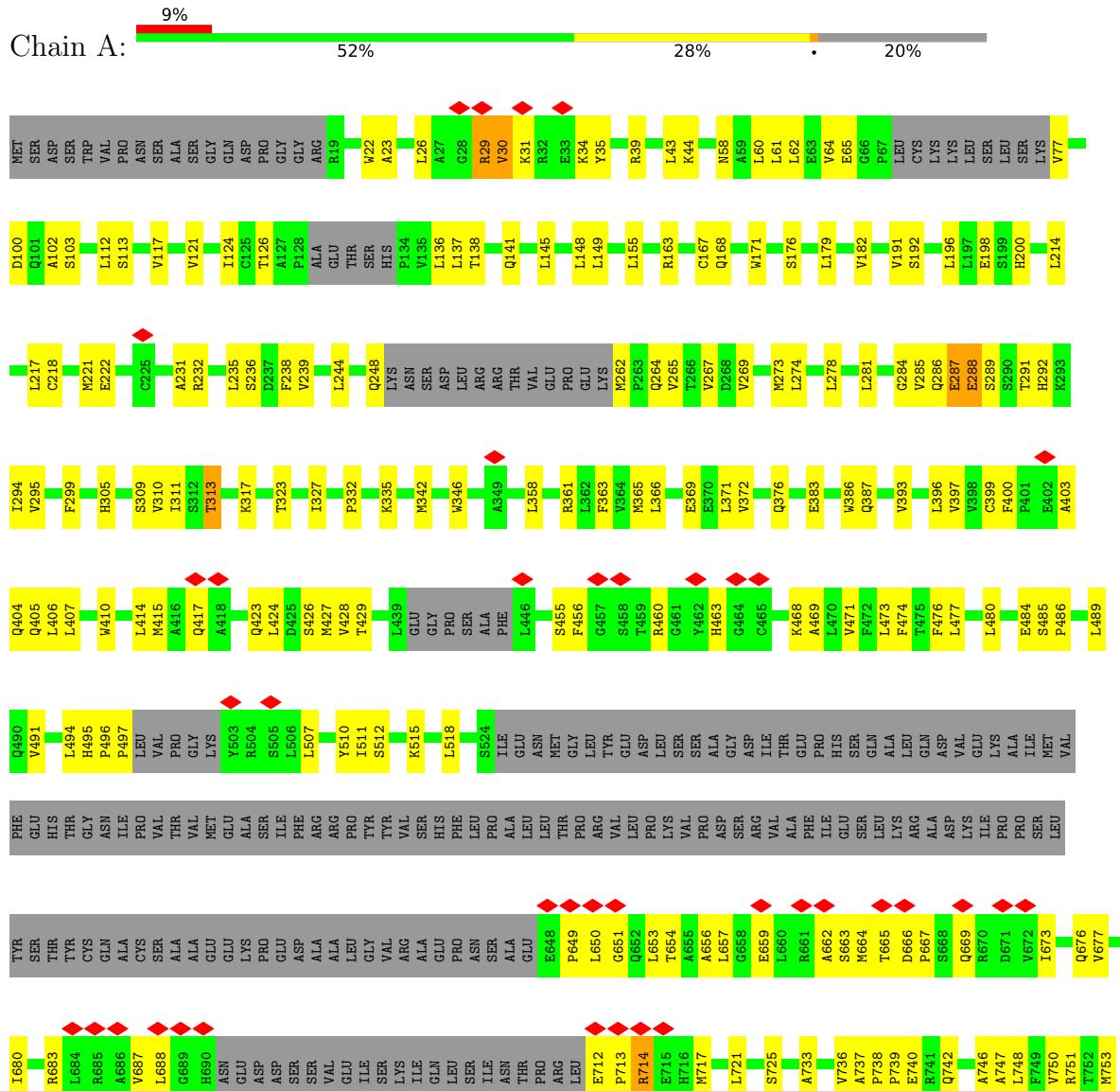
- Molecule 12 is ZINC ION (three-letter code: ZN) (formula: Zn).

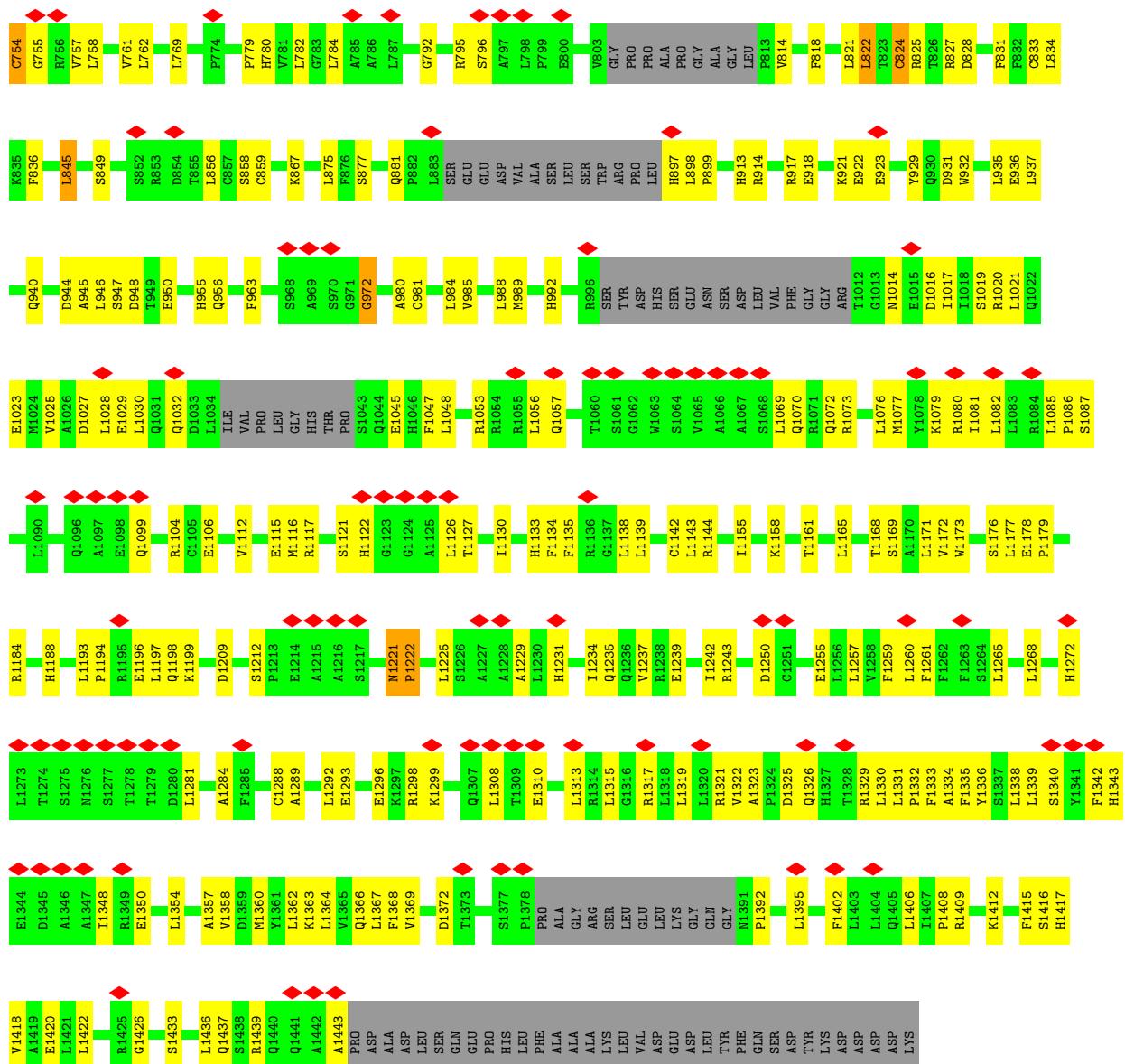
Mol	Chain	Residues	Atoms	AltConf
12	G	1	Total Zn 1 1	0
12	L	2	Total Zn 2 2	0
12	M	2	Total Zn 2 2	0

### 3 Residue-property plots [\(i\)](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

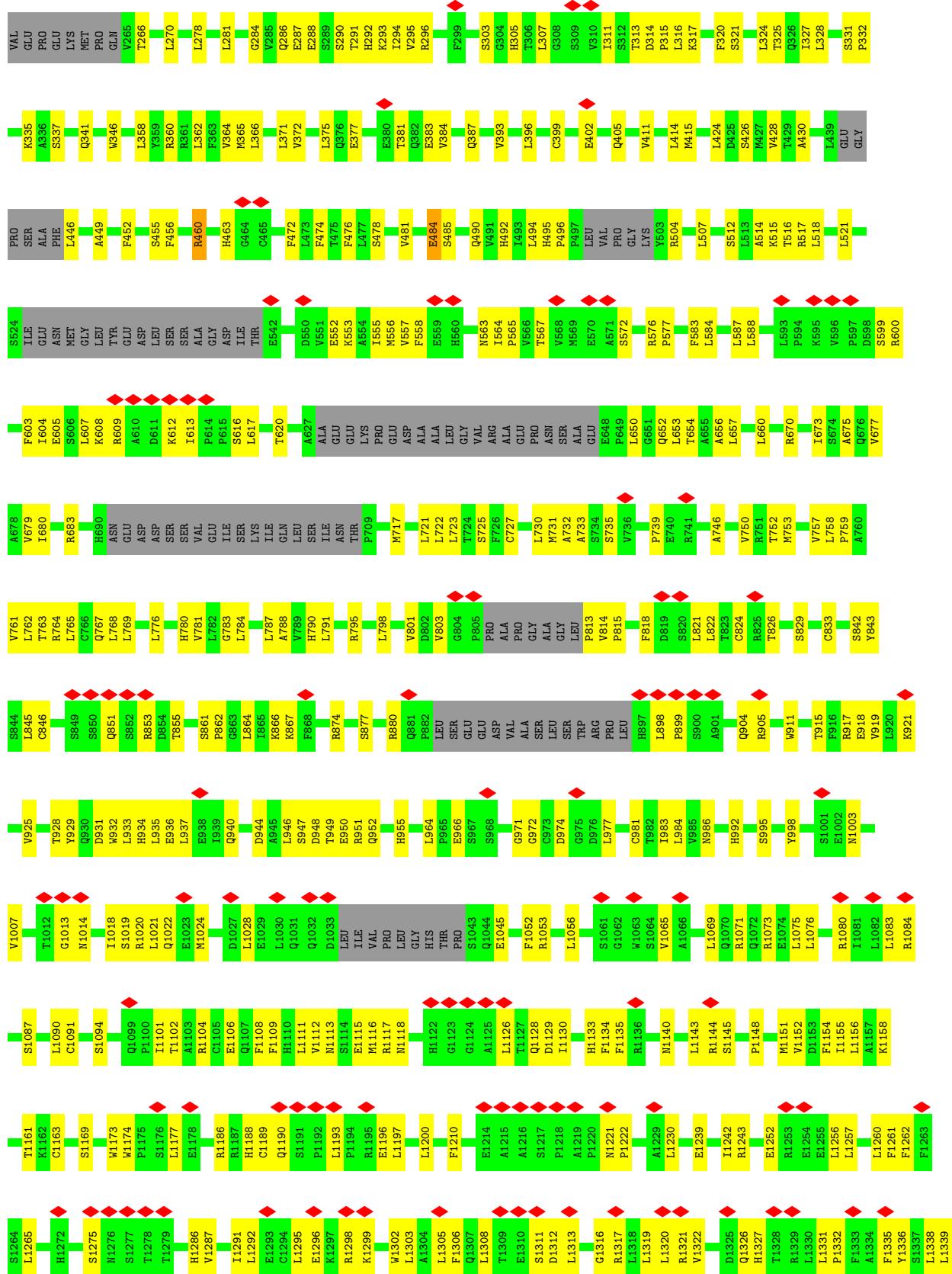
- Molecule 1: Fanconi anemia group A protein

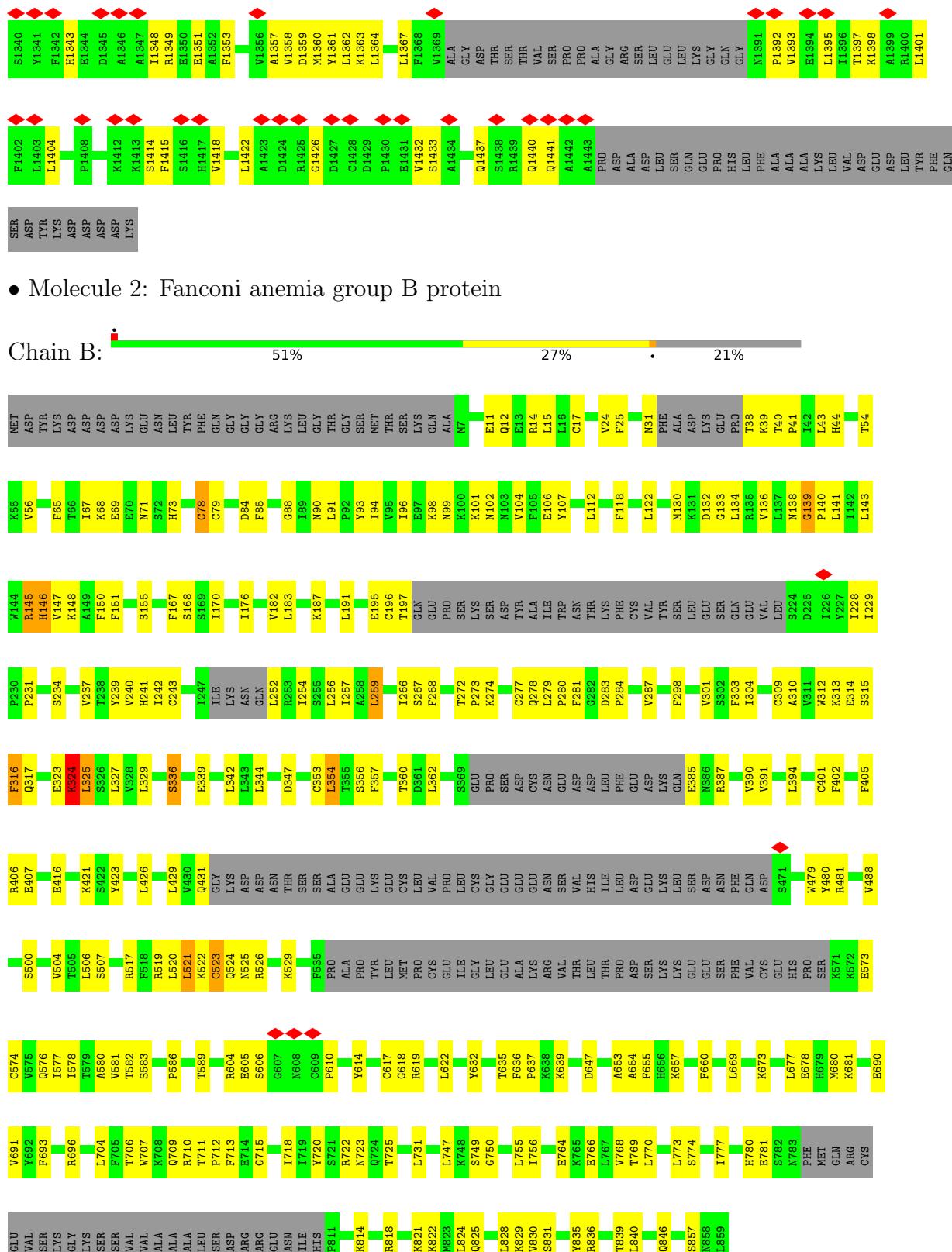




- Molecule 1: Fanconi anemia group A protein



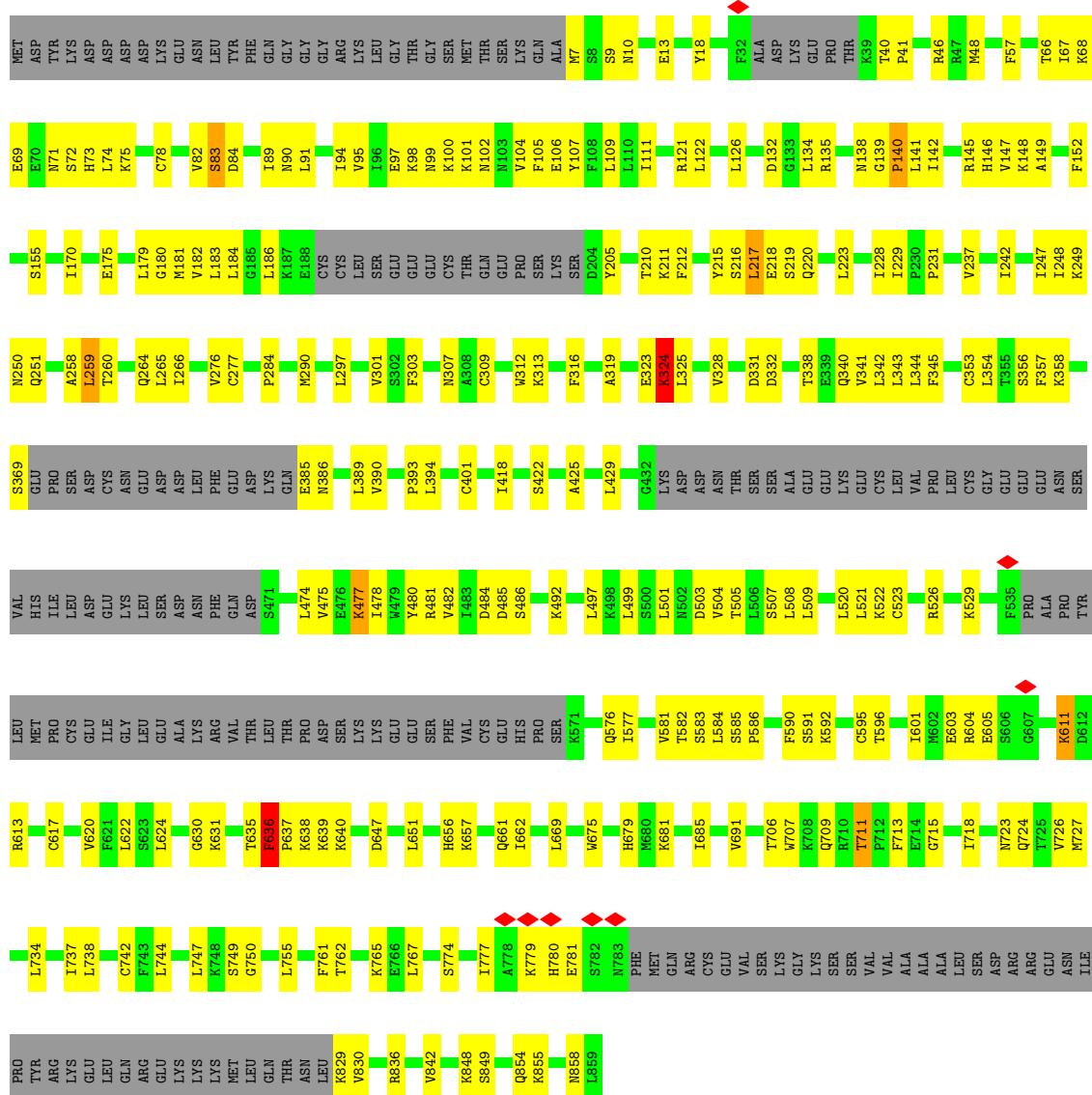




- Molecule 2: Fanconi anemia group B protein

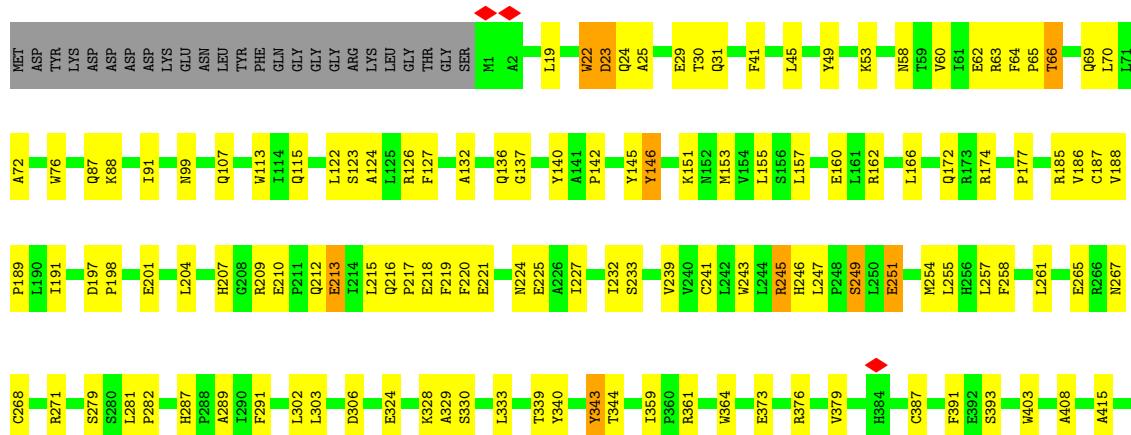
A horizontal bar chart illustrating the distribution of Chain O across four categories. The total length of the bar is 100%.

Category	Percentage
Green	51%
Yellow	27%
Grey	21%



- Molecule 3: Fanconi anemia group C protein

Chain C: 68% • 25% • 6%

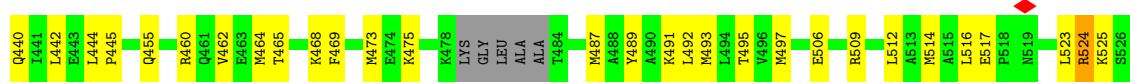
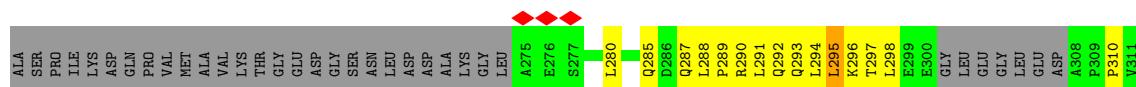
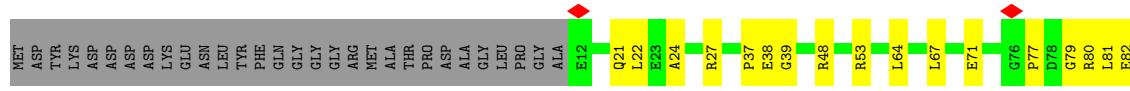




- Molecule 4: Fanconi anemia group E protein

Chain E: 52% 23% • 25%

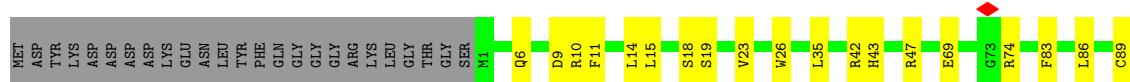
A horizontal progress bar for Chain E. The bar is divided into three colored segments: green (representing 52%), yellow (representing 23%), and grey (representing 25%). A black dot is positioned between the green and yellow segments. The percentage values are labeled next to their respective segments.



- Molecule 5: Fanconi anemia group F protein

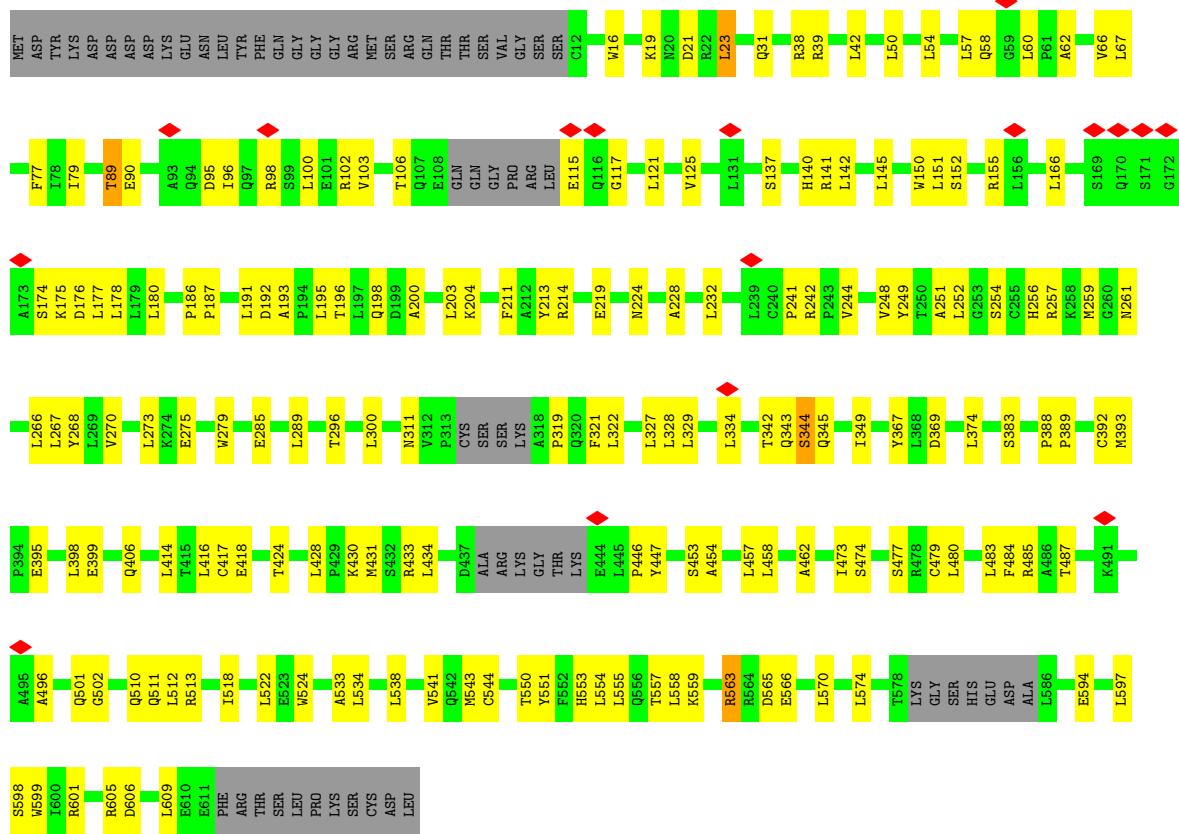
Chain F: 100% completed

A horizontal progress bar for 'Chain F' is shown, consisting of three colored segments: red, green, and grey. The red segment is very small. The green segment is the largest and is labeled '65%' below it. The grey segment is the smallest and is labeled '20%' below it. To the right of the grey segment, the text '15%' is visible, likely representing an additional unlabeled segment.



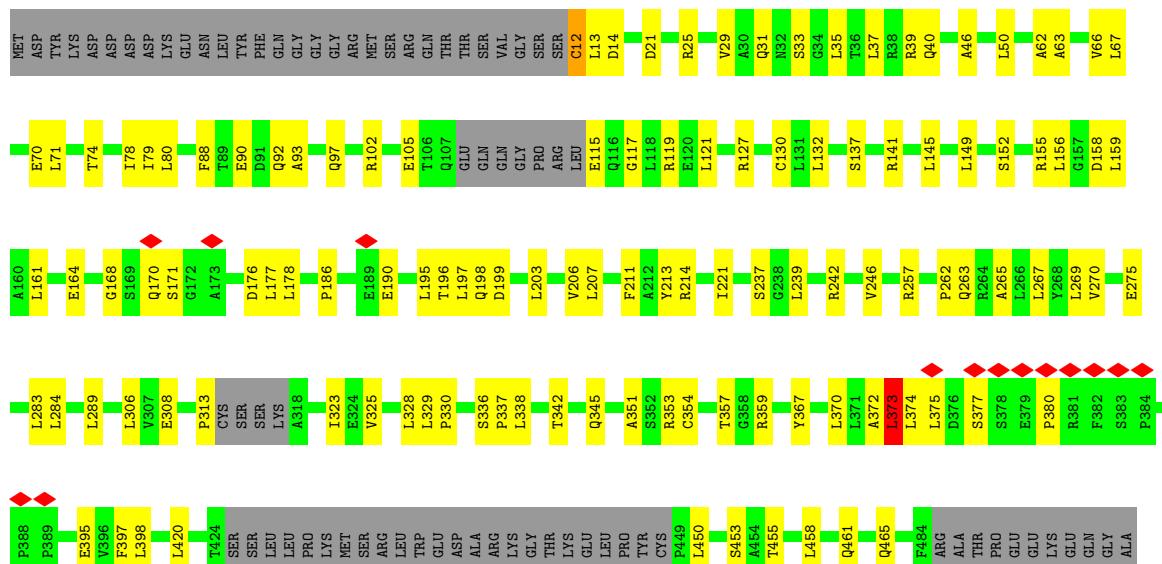
- Molecule 6: Fanconi anemia group G protein

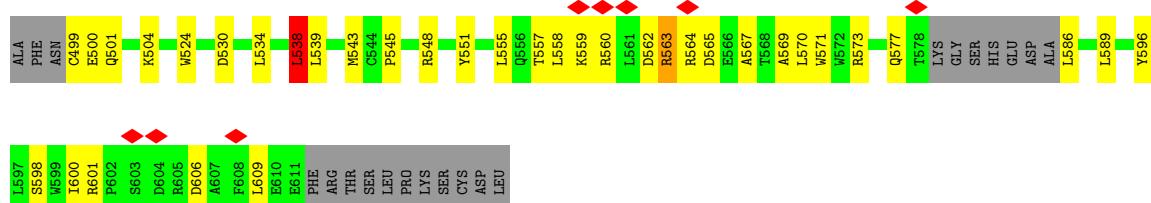
Chain G: 63% 27% 10%



- Molecule 6: Fanconi anemia group G protein

Chain H: 61% 24% 15% 1%

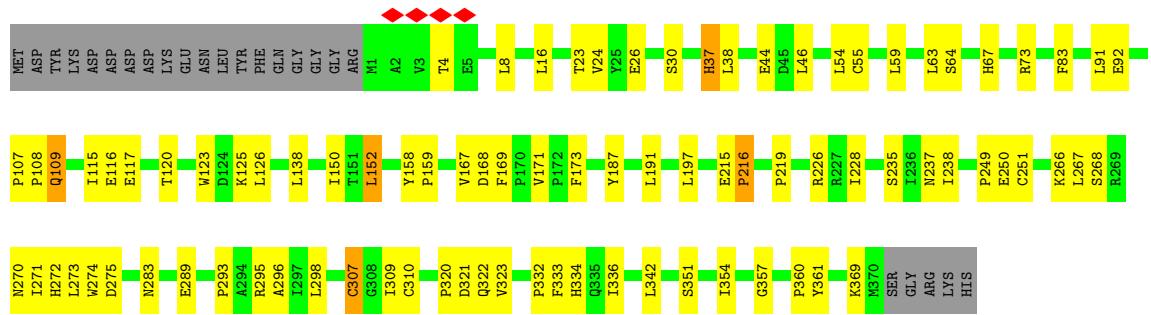




- Molecule 7: E3 ubiquitin-protein ligase FANCL

Chain L: 72% 21% 6%

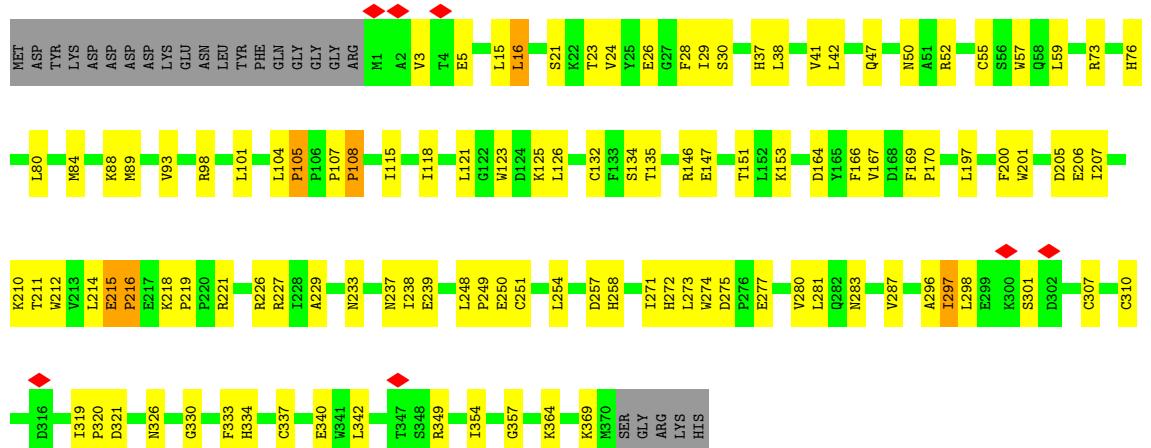
A horizontal progress bar for 'Chain L'. The bar is mostly green, indicating 72% completion. It ends with a yellow section representing 21% and a small orange dot representing 6%. The total length of the bar is 100%.



- Molecule 7: E3 ubiquitin-protein ligase FANCL

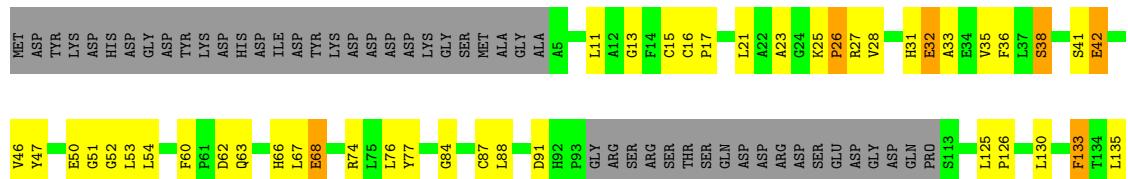
Chain M: 65% 27% • 6%

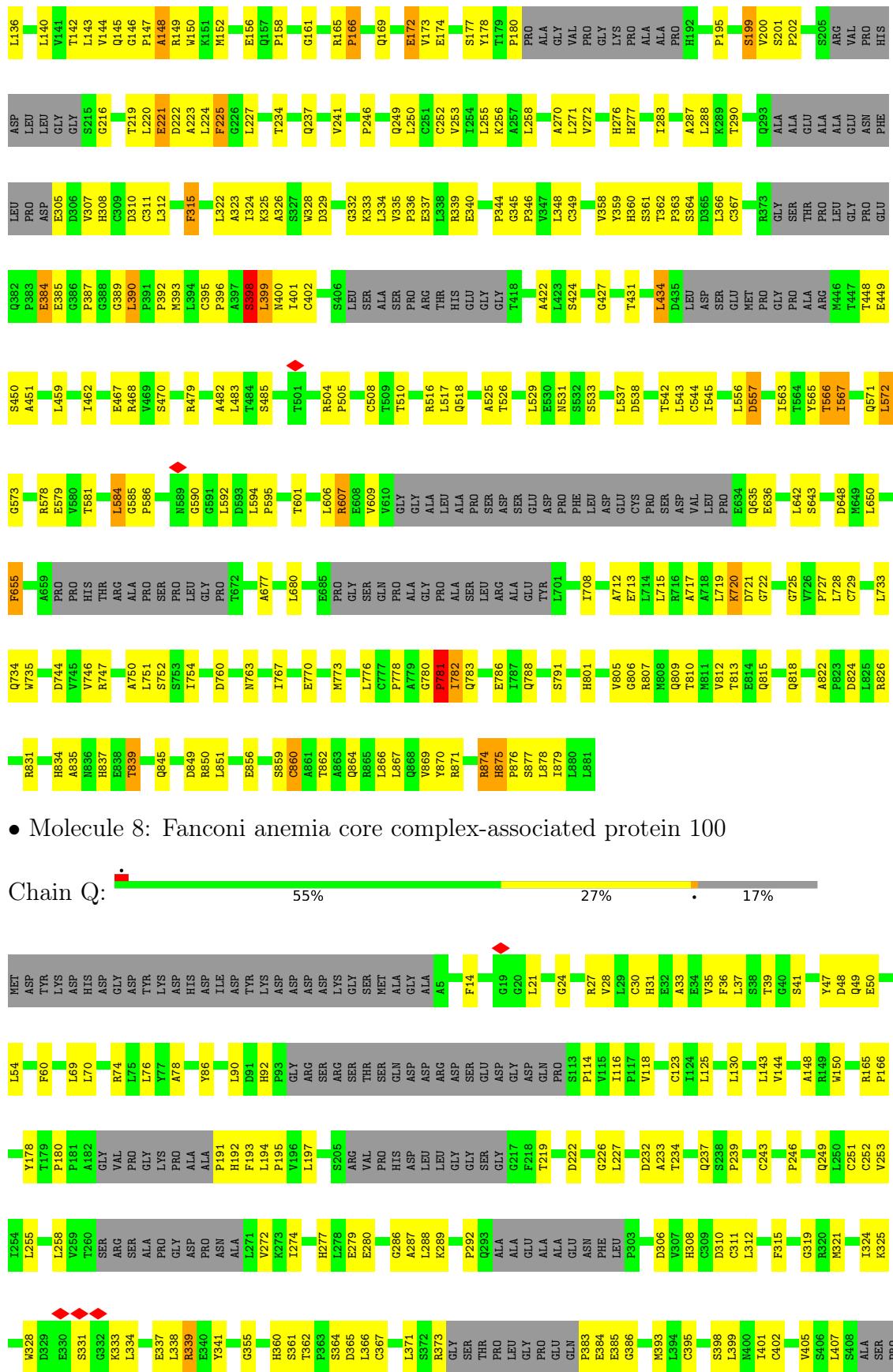
A horizontal progress bar for 'Chain M'. The bar is divided into three segments: a red segment on the left, a green segment in the middle labeled '65%', and a yellow segment on the right labeled '27%'. A small black dot is positioned to the right of the green segment, followed by the text '• 6%'.

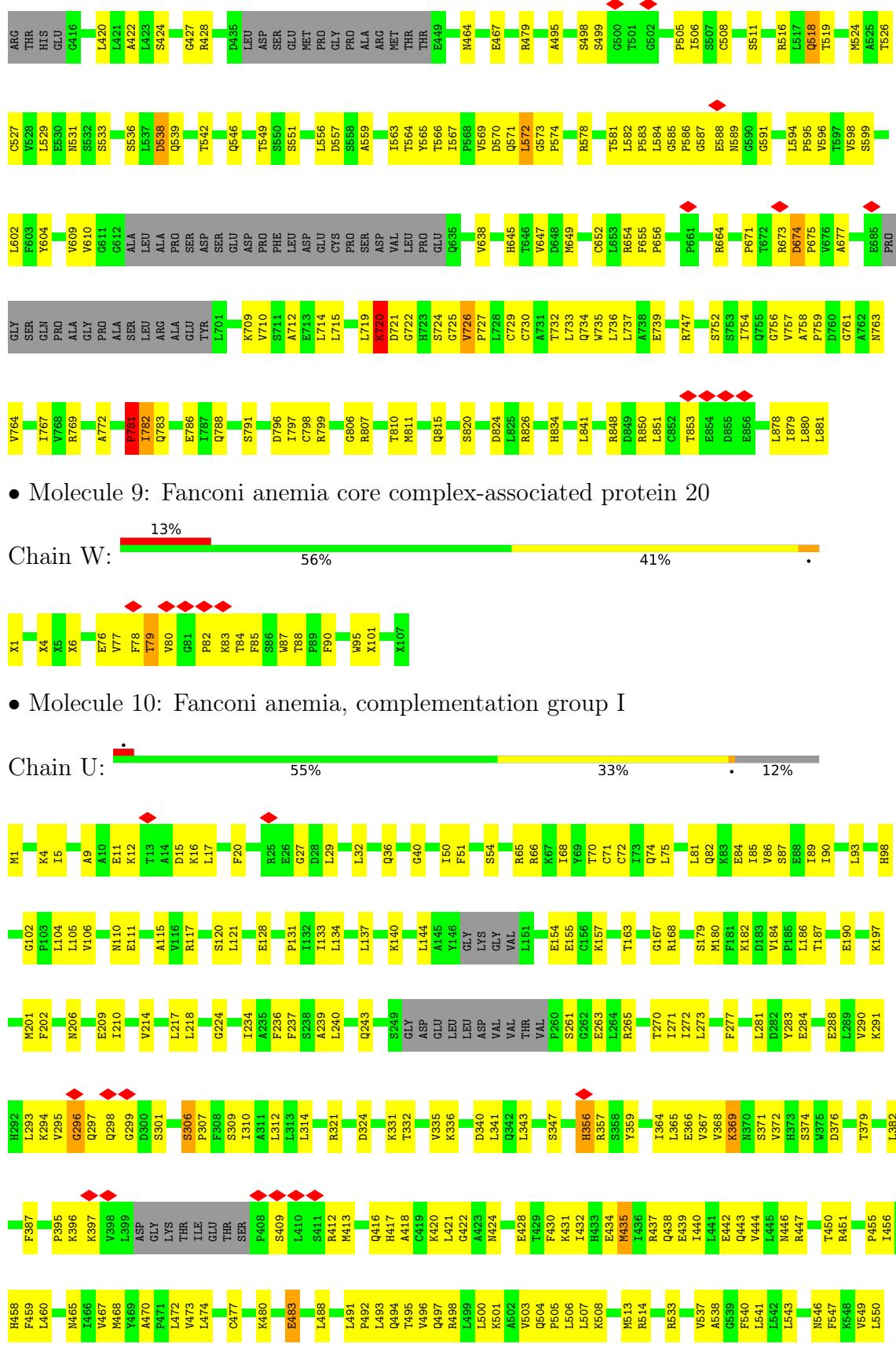


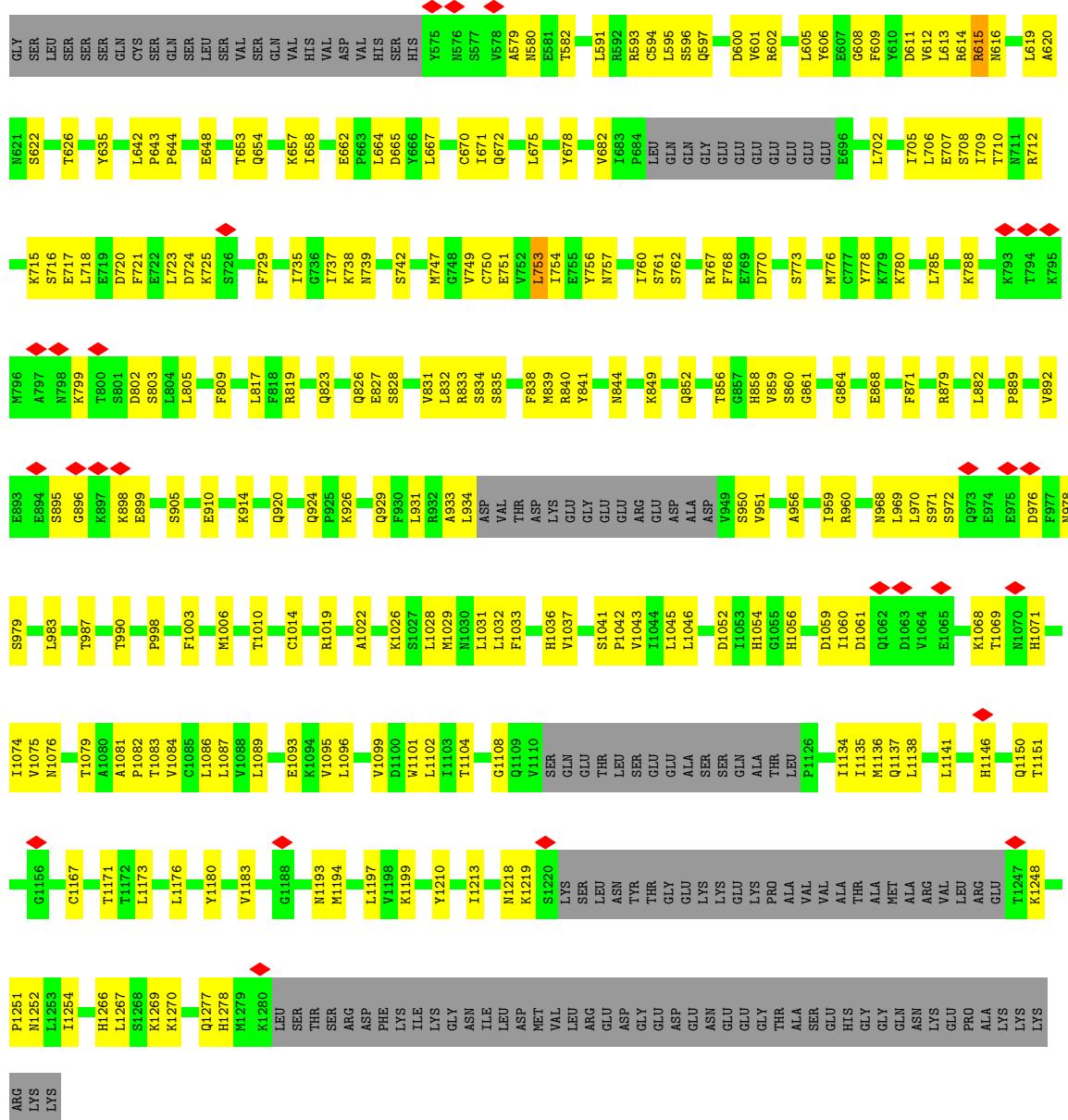
- Molecule 8: Fanconi anemia core complex-associated protein 100

Chain P:  50% 29% • 17%





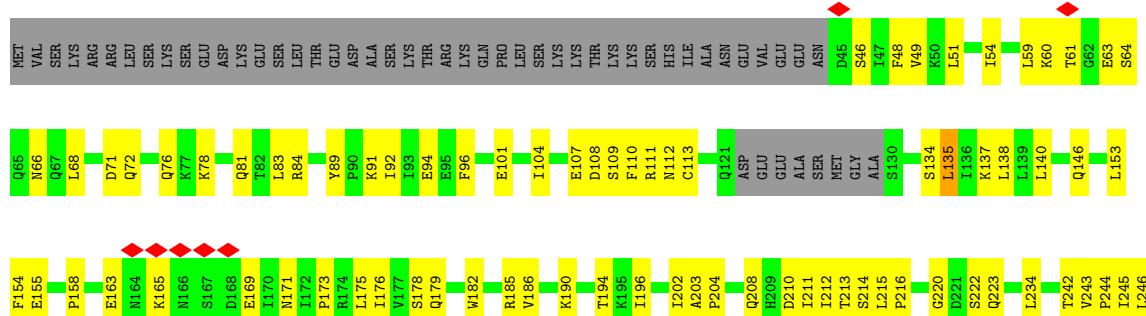


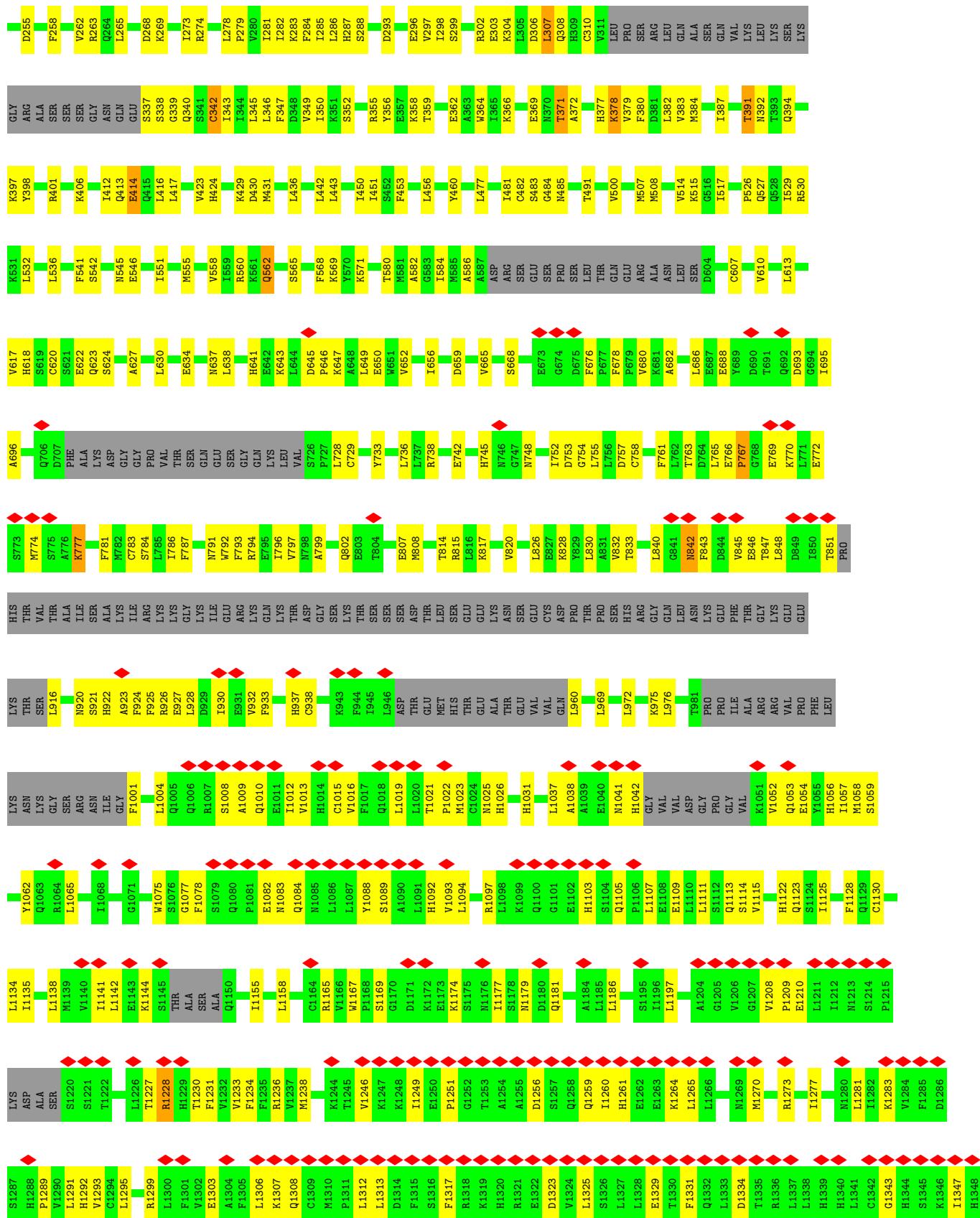


- Molecule 11: Fanconi anemia group D2 protein

A horizontal bar chart illustrating the distribution of Chain V across five categories. The categories are represented by colored segments of a bar, with their respective percentages labeled at the end of each segment.

Category	Percentage
Red	14%
Green	49%
Yellow	30%
Grey	21%





ALA	Q1349
ASP	D1350
GLU	T1351
SER	
GLU	R1352
ASP	L1353
ASP	T1354
MET	
SER	Q1355
SER	H1356
GLN	V1357
ALA	P1358
SER	L1359
LYS	L1360
SER	K1361
LYS	
ALA	K1362
THR	T1363
GLU	A1364
ASP	
GLY	E1365
GLU	L1366
GLU	L1367
ASP	V1368
GLU	C1369
VAL	
SER	R1370
ALA	V1371
GLY	K1372
GLU	A1373
LYS	
GLU	M1374
GLN	
ASP	L1375
SER	T1376
ASP	LEU
GLU	
SER	ASN
TYR	
ASP	CYS
ASP	ARG
ASP	GLU
SER	ALA
ASP	PHE
	TRP
	LEU
	ILE
GLY	
ASN	LEU
ASN	LEU
	LYS
	ASN
	ARG
	ASP
	LEU
	GLN
	GLY
	GLU
	GLU
	ILE
	LYS
	SER
	GLN
	ASN
	SER
	GLN
	GLU
	SER
	THR

## 4 Experimental information i

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76111	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	65	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.071	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0055	Depositor
Map size (Å)	487.63455, 487.63455, 487.63455	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08847, 1.08847, 1.08847	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.40	0/9605	0.55	2/13008 (0.0%)
1	S	0.37	0/10153	0.43	0/13749
2	B	0.82	9/5707 (0.2%)	0.90	4/7686 (0.1%)
2	O	0.49	0/5701	0.69	1/7686 (0.0%)
3	C	0.79	12/4497 (0.3%)	0.79	2/6103 (0.0%)
4	E	0.62	4/3274 (0.1%)	0.73	1/4438 (0.0%)
5	F	0.66	3/2791 (0.1%)	0.73	0/3790
6	G	0.63	2/4568 (0.0%)	0.71	1/6215 (0.0%)
6	H	0.44	0/4293	0.60	2/5840 (0.0%)
7	L	0.73	3/3050 (0.1%)	0.80	2/4143 (0.0%)
7	M	0.48	0/3050	0.67	2/4143 (0.0%)
8	P	0.98	21/5697 (0.4%)	1.01	11/7752 (0.1%)
8	Q	0.46	0/5737	0.67	0/7810
9	W	0.34	0/202	0.44	0/281
10	U	0.42	0/9400	0.55	0/12676
11	V	0.42	0/9433	0.55	0/12760
All	All	0.57	54/87158 (0.1%)	0.67	28/118080 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	9
1	S	0	4
2	B	0	8
2	O	0	4
3	C	0	2
4	E	0	1
6	G	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	H	0	3
7	L	0	2
7	M	0	2
8	P	0	12
8	Q	0	6
10	U	0	4
11	V	0	7
All	All	0	66

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	P	68	GLU	CD-OE1	9.56	1.36	1.25
8	P	68	GLU	CD-OE2	8.94	1.35	1.25
8	P	222	ASP	CG-OD1	8.80	1.45	1.25
3	C	201	GLU	CD-OE2	8.49	1.34	1.25
3	C	225	GLU	CD-OE2	8.34	1.34	1.25
5	F	141	SER	CA-CB	-8.10	1.40	1.52
3	C	221	GLU	CD-OE1	8.10	1.34	1.25
8	P	133	PHE	CG-CD1	-7.62	1.27	1.38
2	B	507	SER	CA-CB	-7.57	1.41	1.52
8	P	216	GLY	C-O	7.26	1.35	1.23
5	F	168	GLU	CD-OE1	7.22	1.33	1.25
2	B	416	GLU	CD-OE1	7.20	1.33	1.25
2	B	314	GLU	CD-OE1	7.16	1.33	1.25
2	B	314	GLU	CD-OE2	7.02	1.33	1.25
3	C	251	GLU	CD-OE2	6.79	1.33	1.25
4	E	100	SER	CA-CB	-6.78	1.42	1.52
8	P	222	ASP	CG-OD2	6.63	1.40	1.25
2	B	407	GLU	CD-OE2	6.61	1.32	1.25
2	B	407	GLU	CD-OE1	6.52	1.32	1.25
8	P	38	SER	CA-CB	-6.51	1.43	1.52
4	E	99	MET	CG-SD	-6.43	1.64	1.81
2	B	336	SER	CA-CB	-6.39	1.43	1.52
3	C	213	GLU	CD-OE2	6.35	1.32	1.25
8	P	398	SER	CA-CB	-6.33	1.43	1.52
2	B	339	GLU	CD-OE2	6.32	1.32	1.25
3	C	249	SER	CA-CB	-6.32	1.43	1.52
7	L	307	CYS	CB-SG	-6.03	1.72	1.82
3	C	218	GLU	CD-OE2	5.97	1.32	1.25
6	G	344	SER	CA-CB	-5.93	1.44	1.52
3	C	221	GLU	CD-OE2	5.92	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	P	172	GLU	CD-OE2	5.86	1.32	1.25
3	C	213	GLU	CD-OE1	5.86	1.32	1.25
5	F	340	GLU	CD-OE1	5.83	1.32	1.25
8	P	359	TYR	CG-CD2	-5.78	1.31	1.39
3	C	201	GLU	CD-OE1	5.73	1.31	1.25
2	B	339	GLU	CD-OE1	5.70	1.31	1.25
6	G	418	GLU	CD-OE1	5.60	1.31	1.25
8	P	358	VAL	CB-CG1	-5.56	1.41	1.52
4	E	38	GLU	CD-OE1	5.50	1.31	1.25
8	P	133	PHE	CB-CG	-5.50	1.42	1.51
3	C	160	GLU	CD-OE1	5.48	1.31	1.25
4	E	71	GLU	CD-OE2	5.38	1.31	1.25
8	P	42	GLU	CD-OE1	5.35	1.31	1.25
8	P	225	PHE	CG-CD1	-5.30	1.30	1.38
8	P	172	GLU	CD-OE1	5.27	1.31	1.25
8	P	360	HIS	CG-ND1	-5.27	1.27	1.38
8	P	310	ASP	CG-OD1	5.26	1.37	1.25
8	P	398	SER	CB-OG	-5.25	1.35	1.42
3	C	204	LEU	C-O	-5.22	1.13	1.23
7	L	92	GLU	CD-OE1	5.16	1.31	1.25
7	L	37	HIS	C-O	-5.14	1.13	1.23
8	P	156	GLU	CD-OE1	5.09	1.31	1.25
8	P	348	LEU	C-O	-5.01	1.13	1.23
8	P	13	GLY	C-O	-5.00	1.15	1.23

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	P	359	TYR	CB-CG-CD2	-7.40	116.56	121.00
3	C	245	ARG	NE-CZ-NH2	-7.01	116.79	120.30
8	P	315	PHE	CB-CA-C	-6.79	96.82	110.40
2	B	324	LYS	CB-CG-CD	6.61	128.80	111.60
8	P	874	ARG	NE-CZ-NH1	6.46	123.53	120.30
6	G	417	CYS	CA-CB-SG	-6.42	102.45	114.00
8	P	359	TYR	CB-CG-CD1	6.37	124.82	121.00
8	P	874	ARG	NE-CZ-NH2	-6.21	117.19	120.30
2	B	406	ARG	NE-CZ-NH1	-6.21	117.19	120.30
4	E	96	ARG	NE-CZ-NH2	6.17	123.38	120.30
8	P	542	THR	CA-CB-OG1	-6.04	96.31	109.00
2	O	474	LEU	CA-CB-CG	5.94	128.96	115.30
2	B	480	TYR	CB-CG-CD1	-5.92	117.45	121.00
8	P	434	LEU	CB-CG-CD2	-5.88	101.01	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	P	222	ASP	CB-CG-OD2	-5.77	113.11	118.30
8	P	566	THR	CB-CA-C	-5.72	96.16	111.60
8	P	26	PRO	N-CD-CG	-5.68	94.67	103.20
7	L	26	GLU	OE1-CD-OE2	-5.61	116.57	123.30
7	M	16	LEU	CA-CB-CG	5.53	128.01	115.30
8	P	221	GLU	CB-CA-C	-5.46	99.48	110.40
6	H	538	LEU	CA-CB-CG	5.41	127.75	115.30
3	C	245	ARG	NE-CZ-NH1	5.37	122.98	120.30
6	H	373	LEU	CA-CB-CG	5.36	127.63	115.30
1	A	822	LEU	CA-CB-CG	-5.24	103.25	115.30
7	M	16	LEU	CB-CG-CD1	-5.16	102.23	111.00
1	A	736	VAL	C-N-CA	-5.10	108.96	121.70
7	L	91	LEU	CB-CG-CD2	-5.05	102.41	111.00
2	B	336	SER	CB-CA-C	-5.00	100.59	110.10

There are no chirality outliers.

All (66) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1221	ASN	Peptide
1	A	1350	GLU	Peptide
1	A	138	THR	Peptide
1	A	313	THR	Peptide
1	A	484	GLU	Peptide
1	A	824	CYS	Peptide
1	A	899	PRO	Peptide
1	A	922	GLU	Peptide
1	A	923	GLU	Peptide
2	B	139	GLY	Peptide
2	B	145	ARG	Peptide
2	B	146	HIS	Peptide
2	B	191	LEU	Peptide
2	B	259	LEU	Peptide
2	B	324	LYS	Peptide
2	B	618	GLY	Peptide
2	B	636	PHE	Peptide
3	C	172	GLN	Peptide
3	C	22	TRP	Peptide
4	E	352	SER	Peptide
6	G	496	ALA	Peptide
6	G	563	ARG	Peptide
6	H	132	LEU	Peptide

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Mol	Chain	Res	Type	Group
6	H	186	PRO	Peptide
6	H	563	ARG	Peptide
7	L	109	GLN	Peptide
7	L	215	GLU	Peptide
7	M	215	GLU	Peptide
7	M	296	ALA	Peptide
2	O	259	LEU	Peptide
2	O	324	LYS	Peptide
2	O	636	PHE	Peptide
2	O	711	THR	Peptide
8	P	146	GLY	Peptide
8	P	329	ASP	Peptide
8	P	345	GLY	Peptide
8	P	389	GLY	Peptide
8	P	398	SER	Peptide
8	P	584	LEU	Peptide
8	P	594	LEU	Peptide
8	P	62	ASP	Peptide
8	P	725	GLY	Peptide
8	P	780	GLY	Peptide
8	P	781	PRO	Peptide
8	P	878	LEU	Peptide
8	Q	584	LEU	Peptide
8	Q	594	LEU	Peptide
8	Q	647	VAL	Peptide
8	Q	720	LYS	Peptide
8	Q	726	VAL	Peptide
8	Q	781	PRO	Peptide
1	S	1221	ASN	Peptide
1	S	1222	PRO	Peptide
1	S	29	ARG	Peptide
1	S	484	GLU	Peptide
10	U	224	GLY	Peptide
10	U	492	PRO	Peptide
10	U	717	GLU	Peptide
10	U	802	ASP	Peptide
11	V	1169	SER	Peptide
11	V	204	PRO	Peptide
11	V	391	THR	Peptide
11	V	483	SER	Peptide
11	V	484	GLY	Peptide
11	V	541	PHE	Peptide

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Mol	Chain	Res	Type	Group
11	V	842	ASN	Peptide

## 5.2 Too-close contacts [\(i\)](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9402	9487	9431	310	0
1	S	9933	10028	9969	345	0
2	B	5605	5790	5768	186	0
2	O	5594	5759	5740	182	0
3	C	4396	4442	4427	128	0
4	E	3224	3390	3384	107	0
5	F	2726	2740	2729	66	0
6	G	4483	4537	4523	126	0
6	H	4216	4288	4273	105	0
7	L	2974	2977	2972	60	0
7	M	2974	2977	2972	97	0
8	P	5598	5681	5652	227	0
8	Q	5631	5724	5694	191	0
9	W	271	242	195	16	0
10	U	9256	9626	9595	315	0
11	V	9258	9475	9422	329	0
12	G	1	0	0	0	0
12	L	2	0	0	0	0
12	M	2	0	0	0	0
All	All	85546	87163	86746	2627	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

All (2627) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:V:586:ALA:HB1	11:V:645:ASP:CB	1.70	1.20
11:V:586:ALA:CB	11:V:645:ASP:HB2	1.76	1.15
11:V:637:ASN:O	11:V:641:HIS:ND1	1.85	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:362:LEU:O	8:P:468:ARG:NH2	1.94	1.01
10:U:261:SER:O	10:U:265:ARG:HG2	1.62	0.99
11:V:647:LYS:O	11:V:650:GLU:HG3	1.62	0.98
7:M:107:PRO:HG3	2:O:401:CYS:SG	2.09	0.92
11:V:930:ILE:HG22	11:V:1019:LEU:HD21	1.51	0.92
2:B:523:CYS:HG	2:B:582:THR:HG1	1.09	0.91
3:C:224:ASN:OD1	3:C:243:TRP:HH2	1.54	0.89
8:P:544:CYS:SG	8:P:601:THR:OG1	2.28	0.89
8:P:467:GLU:O	8:P:470:SER:OG	1.89	0.89
3:C:243:TRP:HZ3	3:C:249:SER:OG	1.57	0.88
3:C:142:PRO:HA	3:C:145:TYR:CE2	2.07	0.88
11:V:508:MET:SD	11:V:545:ASN:ND2	2.47	0.87
10:U:729:PHE:HB2	10:U:788:LYS:HD2	1.57	0.86
11:V:618:HIS:O	11:V:622:GLU:HG3	1.74	0.86
2:O:277:CYS:HB2	2:O:316:PHE:HB3	1.58	0.86
2:O:484:ASP:OD1	2:O:486:SER:OG	1.93	0.86
7:M:107:PRO:HG2	7:M:108:PRO:HD3	1.56	0.85
7:M:297:ILE:HG13	7:M:301:SER:HA	1.56	0.85
2:O:522:LYS:O	2:O:523:CYS:SG	2.35	0.84
8:P:720:LYS:O	8:P:722:GLY:N	2.09	0.84
8:P:290:THR:OG1	8:P:325:LYS:NZ	2.10	0.84
3:C:243:TRP:HZ3	3:C:249:SER:HG	0.89	0.84
6:G:511:GLN:NE2	6:G:544:CYS:SG	2.50	0.83
2:O:146:HIS:O	2:O:148:LYS:N	2.11	0.83
7:L:266:LYS:HD3	7:L:289:GLU:HB2	1.61	0.83
11:V:637:ASN:HB3	11:V:641:HIS:HE1	1.42	0.82
4:E:318:GLU:HA	7:M:76:HIS:HE1	1.44	0.82
1:S:1156:LEU:HD23	1:S:1196:GLU:HB3	1.60	0.82
3:C:241:CYS:SG	4:E:37:PRO:CD	2.67	0.82
2:B:69:GLU:OE1	2:B:71:ASN:ND2	2.13	0.82
8:P:566:THR:O	8:P:566:THR:OG1	1.90	0.82
2:B:88:GLY:HA2	8:P:15:CYS:SG	2.18	0.82
3:C:241:CYS:SG	4:E:37:PRO:HG3	2.20	0.82
6:H:559:LYS:HD2	6:H:563:ARG:HG2	1.62	0.82
2:B:68:LYS:O	2:B:69:GLU:HG3	1.80	0.81
2:B:423:TYR:CG	8:P:606:LEU:HD13	2.14	0.81
5:F:294:TRP:NE1	5:F:349:ASP:OD2	2.13	0.81
6:H:262:PRO:HB3	6:H:289:LEU:HD21	1.61	0.81
4:E:356:SER:OG	4:E:359:ASN:ND2	2.13	0.81
3:C:212:GLN:HE21	3:C:212:GLN:HA	1.46	0.80
5:F:289:LEU:O	6:G:485:ARG:NH1	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:215:GLU:HG2	7:M:319:ILE:HG13	1.63	0.80
8:P:361:SER:OG	8:P:398:SER:O	1.99	0.80
6:H:283:LEU:HB2	6:H:306:LEU:HD13	1.63	0.80
2:O:509:LEU:HD22	8:Q:542:THR:HG21	1.63	0.80
8:P:585:GLY:HA2	8:P:592:LEU:HD11	1.61	0.80
2:B:710:ARG:HD2	2:B:711:THR:HG23	1.62	0.80
3:C:140:TYR:CE2	5:F:169:LEU:HD22	2.17	0.80
2:O:75:LYS:HB3	2:O:97:GLU:HB3	1.63	0.80
1:S:31:LYS:HB2	1:S:34:LYS:HD3	1.64	0.79
3:C:333:LEU:HD11	4:E:48:ARG:HE	1.46	0.79
2:B:98:LYS:HB3	2:B:106:GLU:HB2	1.64	0.78
1:S:822:LEU:HD13	1:S:867:LYS:HD3	1.66	0.78
1:A:497:PRO:HB2	1:A:507:LEU:HD21	1.66	0.78
2:B:309:CYS:SG	2:B:310:ALA:N	2.56	0.78
4:E:80:ARG:NH2	4:E:81:LEU:O	2.16	0.77
2:B:846:GLN:HE22	8:P:877:SER:HB3	1.48	0.77
1:S:1155:ILE:HD13	1:S:1158:LYS:HZ1	1.48	0.77
2:B:506:LEU:H	2:B:525:ASN:HD21	1.30	0.77
8:Q:234:THR:O	8:Q:237:GLN:NE2	2.17	0.77
1:A:650:LEU:HD21	1:A:714:ARG:HH22	1.48	0.77
1:A:1082:LEU:HD11	1:A:1130:ILE:HG22	1.66	0.77
2:B:257:ILE:HD11	2:B:287:VAL:HG21	1.66	0.77
1:S:1336:TYR:OH	1:S:1357:ALA:O	2.01	0.77
11:V:1031:HIS:NE2	11:V:1058:MET:O	2.15	0.77
1:A:1422:LEU:HD12	1:A:1426:GLY:HA3	1.67	0.77
8:Q:24:GLY:O	8:Q:27:ARG:NH1	2.18	0.76
4:E:336:LEU:O	4:E:371:ARG:NH2	2.18	0.76
8:P:571:GLN:O	8:P:573:GLY:N	2.17	0.76
10:U:835:SER:CB	10:U:838:PHE:HB3	2.14	0.76
3:C:224:ASN:OD1	3:C:243:TRP:CH2	2.38	0.76
11:V:1264:LYS:HE3	11:V:1312:LEU:HD22	1.67	0.76
7:L:150:ILE:HG13	7:L:167:VAL:HG22	1.68	0.76
8:P:11:LEU:HD22	8:P:52:GLY:HA3	1.65	0.76
11:V:920:ASN:HA	11:V:924:PHE:HB2	1.68	0.76
2:O:829:LYS:N	8:Q:824:ASP:O	2.18	0.75
3:C:241:CYS:SG	4:E:37:PRO:CG	2.74	0.75
8:Q:516:ARG:NH1	8:Q:519:THR:O	2.16	0.75
3:C:122:LEU:O	5:F:140:ARG:NE	2.20	0.75
1:A:511:ILE:HG22	1:A:515:LYS:HE2	1.68	0.74
8:Q:165:ARG:HG3	8:Q:166:PRO:HD2	1.69	0.74
1:A:281:LEU:HD21	1:A:295:VAL:HG11	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:141:ARG:HH11	6:H:199:ASP:HA	1.52	0.74
10:U:340:ASP:OD2	10:U:357:ARG:NH2	2.20	0.74
1:A:948:ASP:OD2	1:S:1080:ARG:NH1	2.20	0.74
2:B:481:ARG:NH1	2:B:647:ASP:OD1	2.20	0.74
2:B:500:SER:O	2:B:604:ARG:NH1	2.20	0.74
1:S:228:ALA:HB1	1:S:232:ARG:HH21	1.52	0.74
6:G:96:ILE:HG23	6:G:142:LEU:HD21	1.70	0.73
11:V:586:ALA:HB1	11:V:645:ASP:HB2	0.82	0.73
8:P:362:THR:HG23	8:P:364:SER:H	1.53	0.73
1:S:861:SER:HB2	1:S:864:LEU:HD23	1.70	0.73
4:E:293:GLN:HG3	4:E:294:LEU:HD12	1.70	0.73
2:O:69:GLU:OE1	2:O:71:ASN:ND2	2.22	0.73
7:M:101:LEU:HD23	8:Q:386:GLY:HA2	1.70	0.73
7:M:354:ILE:HG12	7:M:369:LYS:HG2	1.69	0.73
11:V:68:LEU:HD13	11:V:72:GLN:HE22	1.54	0.73
1:A:309:SER:O	8:P:831:ARG:NH2	2.22	0.72
2:O:590:PHE:O	2:O:591:SER:OG	2.06	0.72
2:O:40:THR:OG1	2:O:69:GLU:O	2.07	0.72
11:V:1174:LYS:HD3	11:V:1177:ILE:HD12	1.71	0.72
8:P:165:ARG:NE	8:P:166:PRO:HD2	2.05	0.72
3:C:177:PRO:HG3	3:C:210:GLU:OE1	1.89	0.72
6:G:242:ARG:NH1	6:G:275:GLU:O	2.23	0.72
11:V:558:VAL:HG22	11:V:562:GLN:HE22	1.54	0.72
3:C:207:HIS:O	4:E:92:ARG:NH2	2.22	0.72
4:E:287:GLN:OE1	4:E:290:ARG:NH1	2.23	0.72
7:L:216:PRO:HB2	7:L:219:PRO:HB3	1.70	0.72
10:U:115:ALA:HB1	10:U:121:LEU:HD21	1.70	0.72
5:F:122:ARG:NH2	5:F:130:GLN:OE1	2.23	0.72
6:H:284:LEU:HG	6:H:306:LEU:HD21	1.71	0.72
8:P:362:THR:OG1	8:P:363:PRO:HD2	1.89	0.72
11:V:1256:ASP:HB3	11:V:1260:ILE:HD11	1.70	0.72
8:Q:709:LYS:HB2	8:Q:879:ILE:HG23	1.72	0.72
2:B:277:CYS:HB2	2:B:316:PHE:HB3	1.72	0.71
1:A:1313:LEU:HD13	1:A:1317:ARG:HG3	1.72	0.71
4:E:525:LYS:HD2	11:V:155:GLU:HB3	1.72	0.71
7:M:104:LEU:HD12	7:M:105:PRO:CD	2.19	0.71
6:G:416:LEU:HD12	1:S:22:TRP:HZ3	1.56	0.71
8:Q:715:LEU:O	8:Q:719:LEU:N	2.21	0.71
2:O:481:ARG:NH1	2:O:647:ASP:OD1	2.23	0.71
2:O:520:LEU:HD12	8:Q:567:ILE:HG12	1.70	0.71
8:Q:341:TYR:OH	8:Q:385:GLU:O	2.08	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:192:SER:OG	1:S:195:GLU:OE1	2.08	0.71
2:B:102:ASN:HB3	2:B:104:VAL:HG22	1.72	0.70
10:U:622:SER:O	10:U:626:THR:OG1	2.08	0.70
1:A:415:MET:HE1	1:A:427:MET:HA	1.73	0.70
1:S:557:VAL:HG13	1:S:565:PRO:HG2	1.74	0.70
11:V:482:CYS:SG	11:V:517:ILE:HG13	2.31	0.70
11:V:1179:ASN:HB3	11:V:1233:VAL:HG21	1.73	0.70
1:A:512:SER:HA	1:A:515:LYS:HE3	1.72	0.70
8:Q:654:ARG:NH2	8:Q:758:ALA:O	2.24	0.70
2:B:336:SER:O	2:B:336:SER:OG	2.06	0.70
1:A:1319:LEU:HA	1:A:1322:VAL:HG12	1.73	0.70
6:G:431:MET:HG2	6:G:434:LEU:HB2	1.73	0.70
8:Q:371:LEU:HD11	8:Q:384:GLU:HB2	1.73	0.70
1:S:727:CYS:HG	9:W:87:TRP:HE1	1.36	0.70
11:V:928:LEU:HD23	11:V:932:VAL:HG11	1.73	0.70
4:E:516:LEU:HD22	4:E:527:LEU:HD13	1.73	0.70
3:C:29:GLU:OE2	3:C:30:THR:HG23	1.91	0.70
6:G:62:ALA:O	6:G:106:THR:OG1	2.09	0.70
11:V:1125:ILE:HD11	11:V:1134:LEU:HD13	1.72	0.70
1:A:456:PHE:HA	1:A:460:ARG:HB3	1.73	0.70
2:O:492:LYS:HA	2:O:577:ILE:HG22	1.74	0.70
10:U:409:SER:HA	10:U:412:ARG:HE	1.57	0.70
11:V:263:ARG:NH1	11:V:293:ASP:OD2	2.25	0.69
4:E:464:MET:HE3	4:E:468:LYS:HB3	1.74	0.69
1:S:1422:LEU:HD12	1:S:1426:GLY:HA3	1.74	0.69
2:O:781:GLU:HA	8:Q:826:ARG:HD3	1.75	0.69
2:O:520:LEU:HD22	8:P:518:GLN:HB3	1.74	0.69
1:A:22:TRP:O	1:A:26:LEU:HG	1.92	0.69
1:S:332:PRO:HB2	1:S:335:LYS:HE3	1.73	0.69
1:S:186:HIS:HD2	1:S:193:LEU:H	1.38	0.69
3:C:247:LEU:HB2	4:E:132:TRP:NE1	2.08	0.69
2:O:836:ARG:NH2	8:Q:820:SER:O	2.26	0.69
1:S:1422:LEU:HD23	1:S:1437:GLN:HE21	1.57	0.69
7:M:153:LYS:HB2	7:M:164:ASP:HB2	1.75	0.68
10:U:1014:CYS:HA	10:U:1074:ILE:HD12	1.74	0.68
10:U:675:LEU:HD13	10:U:702:LEU:HD22	1.74	0.68
1:A:992:HIS:ND1	1:A:1077:MET:SD	2.59	0.68
6:G:115:GLU:N	6:G:121:LEU:HD21	2.08	0.68
7:L:295:ARG:HD2	7:L:298:LEU:HD21	1.75	0.68
6:G:388:PRO:HG2	8:P:270:ALA:HB1	1.75	0.68
10:U:920:GLN:O	10:U:924:GLN:NE2	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Q:401:ILE:HD11	8:Q:420:LEU:HD22	1.75	0.68
1:A:769:LEU:HB2	1:A:821:LEU:HD22	1.76	0.68
7:L:275:ASP:O	7:L:283:ASN:ND2	2.25	0.68
8:P:67:LEU:O	8:P:68:GLU:HG2	1.92	0.68
1:A:1336:TYR:OH	1:A:1357:ALA:O	2.12	0.68
8:Q:714:LEU:HA	8:Q:815:GLN:HE22	1.59	0.68
1:A:23:ALA:HA	1:A:26:LEU:HD12	1.74	0.68
1:A:1045:GLU:HA	1:A:1104:ARG:HG2	1.76	0.68
8:P:130:LEU:HA	8:P:144:VAL:HA	1.75	0.68
3:C:265:GLU:HG2	3:C:271:ARG:HB2	1.75	0.67
1:S:605:GLU:HB3	1:S:609:ARG:HH12	1.58	0.67
7:L:250:GLU:CD	7:L:250:GLU:N	2.47	0.67
8:Q:130:LEU:HA	8:Q:144:VAL:HA	1.76	0.67
1:A:1027:ASP:O	1:A:1030:LEU:HG	1.94	0.67
3:C:373:GLU:OE1	3:C:376:ARG:NH2	2.27	0.67
5:F:196:LEU:HD11	5:F:201:PHE:HB2	1.76	0.67
1:S:977:LEU:HB3	1:S:1028:LEU:HD21	1.75	0.67
11:V:792:TRP:CE2	11:V:796:ILE:HD11	2.28	0.67
2:B:517:ARG:HH12	2:B:589:THR:HG21	1.59	0.67
6:H:257:ARG:HB2	6:H:289:LEU:HD12	1.77	0.67
11:V:542:SER:HB2	11:V:545:ASN:HD21	1.60	0.67
1:S:1161:THR:O	1:S:1321:ARG:NH2	2.28	0.67
1:S:1336:TYR:HB3	1:S:1395:LEU:HD11	1.77	0.67
10:U:970:LEU:O	10:U:1019:ARG:NH2	2.28	0.67
11:V:1122:HIS:O	11:V:1165:ARG:NH1	2.28	0.67
11:V:515:LYS:HD3	11:V:551:ILE:HG22	1.77	0.67
6:H:79:ILE:HG13	6:H:145:LEU:HD21	1.76	0.67
7:M:216:PRO:HB2	7:M:219:PRO:HB3	1.76	0.67
10:U:417:HIS:HA	10:U:420:LYS:HG2	1.77	0.67
11:V:637:ASN:C	11:V:641:HIS:HD1	1.97	0.67
1:A:218:CYS:HA	1:A:221:MET:HG2	1.76	0.67
2:B:678:GLU:N	2:B:678:GLU:OE1	2.28	0.67
7:M:104:LEU:HD12	7:M:105:PRO:HD3	1.77	0.67
1:A:39:ARG:NH2	6:H:308:GLU:OE1	2.27	0.66
1:A:1336:TYR:O	1:A:1340:SER:OG	2.12	0.66
8:Q:879:ILE:HG22	8:Q:881:LEU:HD13	1.76	0.66
10:U:117:ARG:NH2	10:U:163:THR:O	2.28	0.66
2:B:519:ARG:NH2	2:B:586:PRO:O	2.28	0.66
3:C:212:GLN:HA	3:C:212:GLN:NE2	2.09	0.66
1:S:313:THR:HG22	1:S:317:LYS:HG2	1.78	0.66
10:U:596:SER:HA	10:U:602:ARG:HH21	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:LEU:HD11	1:A:323:THR:HG23	1.75	0.66
1:A:460:ARG:HA	1:A:463:HIS:CD2	2.29	0.66
6:G:39:ARG:NH2	6:G:319:PRO:O	2.28	0.66
7:M:84:MET:HB3	7:M:88:LYS:HZ1	1.60	0.66
2:O:82:VAL:O	2:O:138:ASN:ND2	2.27	0.66
1:S:411:VAL:HG13	1:S:430:ALA:HB1	1.77	0.66
7:M:239:GLU:HB3	7:M:250:GLU:HG2	1.77	0.66
2:O:484:ASP:OD1	2:O:484:ASP:N	2.27	0.66
1:A:468:LYS:HA	1:A:471:VAL:HG23	1.77	0.66
8:Q:546:GLN:HB3	8:Q:564:THR:HG22	1.78	0.66
11:V:1138:LEU:HD23	11:V:1141:ILE:HD11	1.77	0.66
6:H:35:LEU:HD12	6:H:37:LEU:H	1.61	0.66
2:O:503:ASP:OD1	2:O:604:ARG:NH2	2.29	0.66
6:H:214:ARG:NH1	6:H:328:LEU:O	2.28	0.66
2:O:497:LEU:HD21	2:O:504:VAL:HG11	1.77	0.66
1:S:495:HIS:HB3	1:S:496:PRO:HD3	1.76	0.66
7:M:115:ILE:HD11	2:O:394:LEU:HD11	1.77	0.66
1:S:1305:LEU:HA	1:S:1308:LEU:HD21	1.77	0.66
2:B:145:ARG:NH1	2:B:168:SER:O	2.29	0.66
10:U:840:ARG:NH2	10:U:899:GLU:OE2	2.28	0.66
10:U:856:THR:OG1	10:U:858:HIS:O	2.13	0.66
7:M:107:PRO:CG	2:O:401:CYS:SG	2.84	0.66
1:A:780:HIS:O	1:A:784:LEU:HD12	1.95	0.65
2:B:520:LEU:HD12	8:P:567:ILE:HG23	1.76	0.65
2:O:509:LEU:HD23	8:Q:566:THR:HB	1.78	0.65
11:V:64:SER:O	11:V:112:ASN:ND2	2.29	0.65
2:B:431:GLN:NE2	2:B:614:TYR:OH	2.29	0.65
2:B:706:THR:HG22	2:B:718:ILE:HB	1.78	0.65
6:G:19:LYS:O	6:G:23:LEU:HD13	1.95	0.65
6:H:586:LEU:HA	6:H:589:LEU:HD13	1.78	0.65
8:Q:769:ARG:NH1	8:Q:786:GLU:OE2	2.29	0.65
2:B:617:CYS:O	2:B:617:CYS:SG	2.53	0.65
7:M:342:LEU:HD22	7:M:357:GLY:HA3	1.77	0.65
2:O:325:LEU:HA	2:O:344:LEU:O	1.96	0.65
8:P:140:LEU:HD23	8:P:140:LEU:O	1.97	0.65
1:S:456:PHE:HA	1:S:460:ARG:HB3	1.77	0.65
1:S:730:LEU:HD23	1:S:783:GLY:HA2	1.77	0.65
2:B:360:THR:O	2:B:360:THR:OG1	2.11	0.65
3:C:243:TRP:HA	3:C:243:TRP:HE3	1.61	0.65
6:H:221:ILE:HD11	6:H:336:SER:OG	1.97	0.65
1:A:288:GLU:HG3	1:A:292:HIS:CG	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:HIS:HA	2:B:824:LEU:HD21	1.78	0.65
3:C:254:MET:HE1	3:C:257:LEU:HD23	1.79	0.65
11:V:263:ARG:NH2	11:V:288:SER:O	2.30	0.65
11:V:586:ALA:CB	11:V:645:ASP:CB	2.54	0.65
11:V:742:GLU:OE2	11:V:802:GLN:NE2	2.30	0.65
7:L:270:ASN:ND2	7:L:289:GLU:OE2	2.27	0.65
11:V:1115:VAL:HG13	11:V:1138:LEU:HD22	1.78	0.65
2:B:325:LEU:HA	2:B:344:LEU:O	1.97	0.65
3:C:127:PHE:CE1	5:F:147:ARG:HD3	2.31	0.65
4:E:124:ASP:N	4:E:124:ASP:OD1	2.30	0.65
1:A:653:LEU:HA	1:A:683:ARG:HE	1.62	0.65
5:F:116:PHE:HA	5:F:130:GLN:HE21	1.60	0.65
5:F:289:LEU:HD21	6:G:480:LEU:HB3	1.79	0.65
6:H:93:ALA:O	6:H:97:GLN:HG3	1.97	0.65
8:P:543:LEU:HB3	8:P:567:ILE:HG13	1.78	0.65
8:Q:495:ALA:HB1	8:Q:505:PRO:HG3	1.79	0.65
8:Q:781:PRO:O	8:Q:782:ILE:HG12	1.97	0.65
10:U:214:VAL:HA	10:U:217:LEU:HD12	1.79	0.65
10:U:506:LEU:HB3	10:U:513:MET:HE1	1.78	0.65
11:V:345:LEU:O	11:V:349:VAL:HG23	1.96	0.65
1:A:1144:ARG:HH22	1:S:1144:ARG:HH22	1.43	0.64
3:C:243:TRP:HA	3:C:243:TRP:CE3	2.31	0.64
2:O:259:LEU:HB3	2:O:265:LEU:HD12	1.79	0.64
4:E:497:MET:HG2	4:E:512:LEU:HD13	1.79	0.64
8:P:202:PRO:HB3	8:P:225:PHE:CD2	2.32	0.64
1:A:1080:ARG:NH1	1:S:949:THR:O	2.31	0.64
1:A:1143:LEU:HD13	1:A:1188:HIS:HD2	1.62	0.64
8:P:169:GLN:NE2	8:P:172:GLU:OE2	2.29	0.64
10:U:1026:LYS:HD3	10:U:1083:THR:HB	1.79	0.64
1:S:1252:GLU:O	1:S:1298:ARG:NH1	2.30	0.64
2:B:840:LEU:HD21	8:P:812:VAL:HG11	1.80	0.64
4:E:123:GLN:HE22	4:E:130:ASP:H	1.44	0.64
10:U:751:GLU:HA	10:U:754:ILE:HD12	1.78	0.64
2:B:846:GLN:HG3	8:P:874:ARG:NH1	2.13	0.64
8:P:27:ARG:C	8:P:400:ASN:HD21	2.00	0.64
10:U:504:GLN:HA	10:U:507:LEU:HD13	1.79	0.64
8:P:200:VAL:O	8:P:200:VAL:HG12	1.98	0.64
10:U:5:ILE:HG12	10:U:20:PHE:CE2	2.33	0.64
2:B:277:CYS:SG	2:B:278:GLN:N	2.70	0.64
8:Q:720:LYS:C	8:Q:722:GLY:H	1.99	0.64
10:U:749:VAL:O	10:U:753:LEU:HD23	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:524:TRP:HB2	6:G:533:ALA:HB2	1.80	0.64
8:Q:734:GLN:HE21	8:Q:747:ARG:HG2	1.62	0.64
1:S:612:LYS:HB2	1:S:613:ILE:HD12	1.80	0.64
1:A:291:THR:HA	1:A:294:ILE:HD12	1.79	0.63
8:P:746:VAL:HG13	8:P:751:LEU:HD23	1.79	0.63
10:U:1095:VAL:HG11	10:U:1141:LEU:HD11	1.79	0.63
1:A:1168:THR:HA	1:A:1171:LEU:HD12	1.80	0.63
7:M:3:VAL:HG23	7:M:5:GLU:HG2	1.80	0.63
2:O:248:ILE:O	2:O:249:LYS:HG3	1.97	0.63
2:O:499:LEU:HD12	2:O:576:GLN:HG2	1.79	0.63
8:Q:764:VAL:HG12	8:Q:791:SER:HB2	1.80	0.63
10:U:431:LYS:HB2	10:U:432:ILE:HG23	1.80	0.63
2:B:65:PHE:HB2	2:B:118:PHE:CD1	2.33	0.63
2:B:657:LYS:NZ	8:P:557:ASP:OD1	2.32	0.63
8:Q:249:GLN:HB2	8:Q:274:ILE:HD11	1.81	0.63
8:Q:712:ALA:HB3	8:Q:782:ILE:HG22	1.80	0.63
8:Q:772:ALA:HB2	8:Q:783:GLN:HA	1.80	0.63
10:U:956:ALA:HB1	10:U:960:ARG:HH21	1.62	0.63
1:A:366:LEU:HD13	1:A:371:LEU:HD21	1.80	0.63
1:A:1196:GLU:HA	1:A:1199:LYS:HD3	1.80	0.63
2:B:582:THR:HG22	2:B:583:SER:N	2.13	0.63
3:C:41:PHE:CE2	3:C:45:LEU:HD11	2.33	0.63
2:O:82:VAL:HG13	2:O:83:SER:H	1.64	0.63
10:U:117:ARG:HH22	10:U:163:THR:HG22	1.64	0.63
7:L:307:CYS:CB	7:L:310:CYS:SG	2.87	0.63
11:V:526:PRO:HD2	11:V:848:LEU:HD13	1.81	0.63
11:V:752:ILE:O	11:V:755:LEU:N	2.23	0.63
1:A:737:ALA:HB1	1:A:738:PRO:HD2	1.79	0.63
1:A:1366:GLN:HA	1:A:1369:VAL:HG12	1.80	0.63
11:V:623:GLN:OE1	11:V:623:GLN:N	2.28	0.63
10:U:803:SER:OG	10:U:849:LYS:NZ	2.26	0.63
1:S:494:LEU:HD11	1:S:518:LEU:HD21	1.79	0.63
10:U:446:ASN:HD21	11:V:355:ARG:HE	1.46	0.63
5:F:115:LEU:HD23	5:F:129:LEU:HD21	1.80	0.63
2:O:266:ILE:HG12	2:O:276:VAL:HG22	1.80	0.63
8:Q:767:ILE:HG13	8:Q:788:GLN:HB3	1.81	0.63
10:U:105:LEU:HB3	10:U:133:ILE:HG23	1.81	0.63
7:L:307:CYS:HB2	7:L:334:HIS:CE1	2.34	0.62
2:O:475:VAL:HG21	2:O:617:CYS:SG	2.38	0.62
1:S:866:LYS:HD3	1:S:925:VAL:HA	1.81	0.62
1:S:1193:LEU:HD21	1:S:1197:LEU:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:387:PHE:CE2	10:U:443:GLN:HB3	2.35	0.62
11:V:372:ALA:HA	11:V:406:LYS:HZ3	1.65	0.62
8:P:448:THR:O	8:P:451:ALA:N	2.24	0.62
10:U:117:ARG:O	10:U:168:ARG:NH2	2.32	0.62
10:U:442:GLU:OE1	10:U:446:ASN:ND2	2.33	0.62
6:H:461:GLN:HE21	6:H:465:GLN:HE21	1.47	0.62
11:V:645:ASP:O	11:V:649:LEU:HG	1.99	0.62
1:A:1161:THR:O	1:A:1321:ARG:NH2	2.31	0.62
3:C:213:GLU:HA	3:C:213:GLU:OE2	1.99	0.62
10:U:1218:ASN:OD1	10:U:1219:LYS:N	2.33	0.62
6:H:598:SER:HA	6:H:601:ARG:HD3	1.81	0.62
7:M:216:PRO:HG2	7:M:226:ARG:HD3	1.82	0.62
7:M:249:PRO:HG2	7:M:251:CYS:SG	2.40	0.62
11:V:51:LEU:HD23	11:V:54:ILE:HD11	1.82	0.62
4:E:318:GLU:HA	7:M:76:HIS:CE1	2.30	0.62
6:H:206:VAL:HG13	6:H:325:VAL:HG22	1.80	0.62
1:S:1292:LEU:HD12	1:S:1338:LEU:HG	1.82	0.62
10:U:343:LEU:O	10:U:347:SER:OG	2.14	0.62
3:C:213:GLU:OE1	3:C:220:PHE:CE2	2.52	0.62
8:Q:506:ILE:HD13	8:Q:531:ASN:HD22	1.65	0.62
4:E:523:LEU:HD22	11:V:158:PRO:HG3	1.82	0.62
7:L:354:ILE:HG12	7:L:369:LYS:HG2	1.81	0.62
8:Q:710:VAL:HG22	8:Q:880:LEU:HB2	1.81	0.62
1:S:946:LEU:HB3	1:S:950:GLU:HG2	1.82	0.62
1:A:372:VAL:HG21	1:A:406:LEU:HD13	1.81	0.61
1:A:1072:GLN:O	1:A:1076:LEU:HD23	2.00	0.61
1:A:1416:SER:HG	1:A:1417:HIS:CE1	2.18	0.61
2:B:43:LEU:HD13	2:B:96:ILE:HD11	1.81	0.61
2:B:718:ILE:HD11	8:P:556:LEU:HD22	1.82	0.61
6:H:62:ALA:HB2	6:H:102:ARG:HD2	1.81	0.61
1:A:428:VAL:HG22	1:A:476:PHE:CE1	2.35	0.61
7:L:16:LEU:HD11	8:P:483:LEU:HD22	1.82	0.61
2:O:68:LYS:O	2:O:69:GLU:HG3	2.01	0.61
2:O:106:GLU:N	2:O:106:GLU:OE1	2.32	0.61
5:F:19:SER:HB3	5:F:96:ARG:HD2	1.82	0.61
6:H:178:LEU:HD13	6:H:211:PHE:HD2	1.65	0.61
2:O:484:ASP:CG	2:O:485:ASP:H	2.02	0.61
8:P:250:LEU:HD23	8:P:276:HIS:O	1.99	0.61
8:P:398:SER:OG	8:P:422:ALA:HB1	1.99	0.61
8:Q:589:ASN:ND2	8:Q:675:PRO:HD3	2.14	0.61
1:A:100:ASP:O	1:A:103:SER:OG	2.11	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:THR:HG22	1:A:317:LYS:HG3	1.82	0.61
3:C:126:ARG:HH12	5:F:140:ARG:HD3	1.63	0.61
6:H:370:LEU:HA	6:H:373:LEU:HG	1.82	0.61
6:G:555:LEU:HD21	6:G:570:LEU:HB2	1.82	0.61
6:H:119:ARG:HH22	6:H:161:LEU:HB3	1.64	0.61
7:M:107:PRO:N	7:M:108:PRO:HD2	2.16	0.61
8:P:537:LEU:HD23	8:P:572:LEU:HD23	1.82	0.61
11:V:766:GLU:OE2	11:V:770:LYS:NZ	2.25	0.61
1:A:1250:ASP:O	1:A:1298:ARG:NH1	2.33	0.61
3:C:387:CYS:SG	3:C:393:SER:OG	2.57	0.61
10:U:261:SER:O	10:U:265:ARG:CG	2.44	0.61
3:C:123:SER:HA	5:F:140:ARG:NH2	2.16	0.61
6:G:249:TYR:HA	6:G:252:LEU:HD12	1.82	0.61
1:S:555:ILE:HD13	1:S:603:PHE:HB2	1.83	0.61
10:U:272:ILE:HG23	10:U:312:LEU:HD12	1.82	0.61
2:B:283:ASP:HB3	2:B:304:ILE:HD12	1.82	0.61
3:C:449:VAL:O	3:C:453:LEU:HD23	2.01	0.61
7:M:207:ILE:O	7:M:211:THR:OG1	2.18	0.61
7:M:215:GLU:HG2	7:M:319:ILE:CG1	2.30	0.61
2:O:669:LEU:O	2:O:709:GLN:NE2	2.34	0.61
8:P:579:GLU:OE2	8:Q:516:ARG:NH2	2.33	0.61
10:U:493:LEU:HD23	10:U:493:LEU:H	1.65	0.61
6:G:369:ASP:OD1	1:S:29:ARG:HD2	2.01	0.60
8:P:324:ILE:HA	8:P:337:GLU:O	2.01	0.60
11:V:1299:ARG:HH11	11:V:1359:LEU:HD12	1.64	0.60
6:H:499:CYS:SG	6:H:500:GLU:N	2.73	0.60
8:P:424:SER:O	8:P:427:GLY:N	2.32	0.60
1:S:1358:VAL:HG11	1:S:1418:VAL:HG13	1.83	0.60
10:U:751:GLU:OE2	10:U:841:TYR:OH	2.14	0.60
2:B:79:CYS:HA	2:B:93:TYR:CE1	2.36	0.60
2:B:176:ILE:HD12	2:B:182:VAL:HG11	1.82	0.60
11:V:938:CYS:HG	11:V:960:LEU:N	1.99	0.60
2:B:423:TYR:CZ	8:P:606:LEU:HB3	2.36	0.60
3:C:132:ALA:O	3:C:136:GLN:NE2	2.34	0.60
1:S:455:SER:O	1:S:460:ARG:N	2.30	0.60
1:S:1252:GLU:HB3	1:S:1256:LEU:HD22	1.83	0.60
4:E:403:LEU:HB3	4:E:440:GLN:NE2	2.15	0.60
2:O:247:ILE:HG23	2:O:249:LYS:O	2.01	0.60
5:F:202:LEU:HA	5:F:205:ILE:HD12	1.82	0.60
8:Q:674:ASP:HB3	8:Q:677:ALA:H	1.66	0.60
10:U:366:GLU:HA	10:U:369:LYS:HD2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:V:638:LEU:C	11:V:638:LEU:HD23	2.21	0.60
1:A:918:GLU:HA	1:A:921:LYS:HE3	1.84	0.60
1:A:1079:LYS:HD2	1:A:1127:THR:HG21	1.84	0.60
2:B:504:VAL:HG21	2:B:578:ILE:HD13	1.82	0.60
3:C:267:ASN:O	3:C:555:ARG:NH2	2.34	0.60
7:M:23:THR:HG23	7:M:24:VAL:HG23	1.83	0.60
10:U:507:LEU:O	10:U:514:ARG:NH1	2.35	0.60
6:H:555:LEU:HD23	6:H:558:LEU:HD21	1.84	0.60
10:U:508:LYS:HG2	10:U:547:PHE:HE1	1.67	0.60
1:A:795:ARG:NH1	1:A:858:SER:O	2.34	0.60
1:A:1106:GLU:OE1	1:A:1106:GLU:N	2.28	0.60
11:V:451:ILE:HG22	11:V:491:THR:HG21	1.84	0.60
11:V:1360:LEU:O	11:V:1364:LEU:HD13	2.01	0.60
8:P:47:TYR:CE1	8:P:54:LEU:HB3	2.37	0.60
8:P:776:LEU:HD13	8:P:879:ILE:HD12	1.83	0.60
2:O:504:VAL:HG12	2:O:601:ILE:HG12	1.82	0.59
11:V:1123:GLN:O	11:V:1165:ARG:NH2	2.35	0.59
11:V:1167:TRP:O	11:V:1174:LYS:NZ	2.27	0.59
8:Q:726:VAL:HG22	8:Q:727:PRO:HD2	1.85	0.59
10:U:9:ALA:HA	10:U:17:LEU:HD11	1.84	0.59
3:C:191:ILE:HG23	3:C:232:ILE:HD12	1.84	0.59
7:L:16:LEU:HD11	8:P:483:LEU:CD2	2.32	0.59
1:S:171:TRP:NE1	1:S:196:LEU:O	2.32	0.59
1:S:761:VAL:O	1:S:765:LEU:HG	2.02	0.59
1:A:992:HIS:O	1:A:1073:ARG:NH2	2.36	0.59
6:H:213:TYR:HD2	6:H:329:LEU:HD22	1.68	0.59
8:P:234:THR:O	8:P:237:GLN:NE2	2.30	0.59
8:Q:719:LEU:HD11	8:Q:732:THR:HA	1.84	0.59
10:U:1068:LYS:HB3	10:U:1071:HIS:HD2	1.67	0.59
1:A:1171:LEU:HD22	1:A:1229:ALA:HB2	1.85	0.59
7:M:47:GLN:HE22	7:M:50:ASN:HB2	1.67	0.59
11:V:60:LYS:HZ3	11:V:63:GLU:HB3	1.66	0.59
2:B:266:ILE:HD12	2:B:268:PHE:CE2	2.38	0.59
4:E:102:LEU:HD22	4:E:109:LEU:HD11	1.83	0.59
7:L:4:THR:HG23	7:L:8:LEU:HB2	1.85	0.59
7:M:16:LEU:HD11	2:O:422:SER:OG	2.03	0.59
2:O:102:ASN:HB3	2:O:104:VAL:HG22	1.85	0.59
8:Q:536:SER:HB3	8:Q:574:PRO:HD3	1.85	0.59
1:S:730:LEU:HD12	1:S:733:ALA:HB3	1.84	0.59
10:U:5:ILE:HG12	10:U:20:PHE:HE2	1.67	0.59
10:U:438:GLN:HB2	10:U:477:CYS:SG	2.42	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:826:THR:HG23	1:S:829:SER:H	1.68	0.59
1:A:1364:LEU:HD11	1:A:1395:LEU:HD13	1.83	0.59
5:F:160:ASP:OD1	5:F:161:SER:N	2.34	0.59
8:Q:48:ASP:O	8:Q:50:GLU:N	2.35	0.59
10:U:396:LYS:HG3	10:U:397:LYS:HD3	1.85	0.59
10:U:658:ILE:HD11	10:U:738:LYS:HE3	1.85	0.59
11:V:637:ASN:O	11:V:641:HIS:CE1	2.55	0.59
11:V:1295:LEU:HD22	11:V:1353:LEU:HD22	1.85	0.59
8:Q:373:ARG:HH11	8:Q:385:GLU:HA	1.67	0.59
11:V:94:GLU:OE1	11:V:94:GLU:N	2.27	0.59
11:V:738:ARG:HD2	11:V:799:ALA:HA	1.85	0.59
1:A:827:ARG:HD3	1:A:945:ALA:HA	1.85	0.59
1:A:1155:ILE:HD13	1:A:1158:LYS:HZ1	1.67	0.59
8:P:581:THR:O	8:Q:518:GLN:HA	2.03	0.59
8:Q:652:CYS:HB3	8:Q:759:PRO:HB3	1.82	0.59
1:S:1308:LEU:HB3	1:S:1320:LEU:HD21	1.84	0.59
1:A:717:MET:O	1:A:721:LEU:HG	2.03	0.58
1:A:955:HIS:HB3	1:A:1020:ARG:HD2	1.85	0.58
3:C:227:ILE:CD1	3:C:239:VAL:HG12	2.33	0.58
10:U:413:MET:SD	10:U:417:HIS:HD2	2.26	0.58
10:U:593:ARG:HD3	11:V:182:TRP:HZ3	1.68	0.58
1:A:827:ARG:HH21	1:A:944:ASP:H	1.50	0.58
2:B:711:THR:O	2:B:713:PHE:N	2.37	0.58
5:F:18:SER:O	5:F:100:ASN:ND2	2.36	0.58
8:P:607:ARG:NH2	8:P:636:GLU:O	2.35	0.58
1:S:117:VAL:HG13	1:S:148:LEU:HD21	1.84	0.58
1:S:366:LEU:HD13	1:S:371:LEU:HD21	1.83	0.58
1:A:845:LEU:HD11	1:A:913:HIS:CD2	2.39	0.58
2:B:521:LEU:O	2:B:521:LEU:HD23	2.02	0.58
7:L:228:ILE:O	7:L:235:SER:OG	2.15	0.58
8:Q:36:PHE:CD2	8:Q:76:LEU:HD11	2.37	0.58
1:A:117:VAL:HG23	1:A:148:LEU:HD21	1.84	0.58
1:A:1422:LEU:HD23	1:A:1437:GLN:HE21	1.67	0.58
2:O:301:VAL:HB	2:O:309:CYS:SG	2.44	0.58
8:P:77:TYR:CD2	8:P:135:LEU:HD11	2.38	0.58
8:P:133:PHE:C	8:P:133:PHE:CD2	2.73	0.58
10:U:237:PHE:CZ	10:U:271:ILE:HG13	2.38	0.58
10:U:263:GLU:N	10:U:263:GLU:OE1	2.36	0.58
10:U:1068:LYS:HB3	10:U:1071:HIS:CD2	2.37	0.58
11:V:349:VAL:O	11:V:352:SER:OG	2.19	0.58
11:V:793:PHE:HA	11:V:796:ILE:HD12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:100:LEU:HD22	6:G:125:VAL:HG21	1.86	0.58
2:O:46:ARG:NH2	2:O:48:MET:SD	2.75	0.58
8:P:84:GLY:O	8:P:130:LEU:HD21	2.04	0.58
11:V:1325:LEU:O	11:V:1329:GLU:HG2	2.03	0.58
10:U:295:VAL:HG23	10:U:301:SER:HA	1.85	0.58
10:U:379:THR:HA	10:U:382:LEU:HD12	1.85	0.58
2:B:781:GLU:HG2	2:B:830:VAL:HG22	1.85	0.58
4:E:429:LEU:HB3	4:E:460:ARG:HH12	1.67	0.58
8:P:479:ARG:HH21	8:P:479:ARG:HG3	1.69	0.58
8:P:715:LEU:O	8:P:719:LEU:N	2.36	0.58
3:C:448:ALA:O	3:C:452:HIS:ND1	2.35	0.58
8:Q:362:THR:HG23	8:Q:365:ASP:H	1.69	0.58
1:S:650:LEU:HA	1:S:653:LEU:HD12	1.85	0.58
11:V:1236:ARG:HG3	11:V:1293:VAL:HG21	1.86	0.58
1:A:1243:ARG:HA	1:A:1243:ARG:NE	2.19	0.58
4:E:280:LEU:O	4:E:285:GLN:NE2	2.32	0.58
6:G:79:ILE:HD11	6:G:198:GLN:HE21	1.67	0.58
8:Q:720:LYS:HD3	8:Q:725:GLY:HA3	1.85	0.58
1:S:731:MET:O	1:S:735:SER:OG	2.21	0.58
10:U:835:SER:HB3	10:U:838:PHE:HB3	1.85	0.58
1:A:287:GLU:OE1	1:A:287:GLU:N	2.37	0.58
2:B:749:SER:O	2:B:755:LEU:HD11	2.04	0.58
4:E:291:LEU:O	4:E:295:LEU:HD13	2.04	0.58
2:O:139:GLY:O	2:O:141:LEU:N	2.36	0.58
8:P:525:ALA:HB2	8:P:584:LEU:HD11	1.86	0.58
1:S:723:LEU:HD11	9:W:90:PHE:HE1	1.69	0.58
11:V:153:LEU:HG	11:V:176:ILE:HD11	1.86	0.58
11:V:568:PHE:HD2	11:V:851:THR:HG21	1.69	0.58
1:A:417:GLN:OE1	1:A:423:GLN:NE2	2.37	0.57
2:B:690:GLU:OE2	2:B:690:GLU:N	2.35	0.57
5:F:69:GLU:HA	5:F:74:ARG:NH2	2.18	0.57
5:F:151:TYR:CZ	5:F:162:LEU:HD23	2.39	0.57
6:G:140:HIS:HB2	6:G:187:PRO:HG3	1.86	0.57
6:H:538:LEU:HD12	6:H:539:LEU:N	2.19	0.57
7:L:23:THR:HG23	7:L:24:VAL:HG23	1.85	0.57
1:S:313:THR:HG23	1:S:316:LEU:HD23	1.86	0.57
1:S:899:PRO:O	1:S:905:ARG:NH2	2.37	0.57
1:S:929:TYR:HB2	1:S:972:GLY:HA2	1.86	0.57
11:V:306:ASP:O	11:V:308:GLN:NE2	2.37	0.57
11:V:630:LEU:HD13	11:V:843:PHE:HB3	1.84	0.57
11:V:637:ASN:HB3	11:V:641:HIS:CE1	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:955:HIS:NE2	1:A:1016:ASP:OD2	2.34	0.57
1:A:1087:SER:OG	1:A:1133:HIS:O	2.15	0.57
6:G:267:LEU:HB3	1:S:93:PHE:HE2	1.68	0.57
2:O:611:LYS:HD3	2:O:613:ARG:HE	1.69	0.57
10:U:440:ILE:O	10:U:444:VAL:HG23	2.02	0.57
11:V:413:GLN:OE1	11:V:413:GLN:N	2.37	0.57
1:A:35:TYR:CD1	1:A:39:ARG:HG2	2.40	0.57
3:C:186:VAL:O	3:C:186:VAL:HG12	2.03	0.57
4:E:293:GLN:O	4:E:297:THR:HG23	2.03	0.57
10:U:434:GLU:OE1	10:U:434:GLU:N	2.36	0.57
1:A:124:ILE:HD11	1:A:141:GLN:O	2.04	0.57
1:A:1121:SER:O	1:A:1122:HIS:ND1	2.38	0.57
1:S:652:GLN:O	1:S:683:ARG:NH2	2.38	0.57
1:A:1053:ARG:HG3	1:A:1057:GLN:HE21	1.70	0.57
3:C:247:LEU:HB2	4:E:132:TRP:CE2	2.39	0.57
10:U:480:LYS:HA	10:U:483:GLU:OE2	2.05	0.57
10:U:1180:TYR:HA	10:U:1183:VAL:HG12	1.86	0.57
2:B:150:PHE:CE1	2:B:170:ILE:HB	2.39	0.57
2:B:829:LYS:HB3	8:P:824:ASP:HB3	1.85	0.57
2:O:486:SER:HA	2:O:582:THR:O	2.05	0.57
1:S:750:VAL:HG21	1:S:790:HIS:HB3	1.87	0.57
1:S:1332:PRO:HG2	1:S:1367:LEU:HD11	1.86	0.57
2:O:170:ILE:HD11	2:O:183:LEU:HB3	1.87	0.57
8:Q:311:CYS:SG	8:Q:312:LEU:N	2.78	0.57
10:U:4:LYS:HE2	10:U:20:PHE:CZ	2.40	0.57
11:V:1078:PHE:O	11:V:1084:GLN:NE2	2.37	0.57
1:A:1392:PRO:HA	1:A:1395:LEU:HG	1.87	0.57
2:B:582:THR:CG2	2:B:583:SER:N	2.68	0.57
10:U:852:GLN:HG2	10:U:859:VAL:HA	1.87	0.57
2:B:170:ILE:HD11	2:B:183:LEU:HD13	1.87	0.57
6:H:530:ASP:O	6:H:534:LEU:HG	2.04	0.57
8:Q:39:THR:HG1	8:Q:41:SER:HG	1.48	0.57
8:Q:279:GLU:OE1	8:Q:279:GLU:N	2.37	0.57
8:Q:508:CYS:SG	8:Q:527:CYS:SG	3.03	0.57
8:Q:570:ASP:OD1	8:Q:578:ARG:NH2	2.35	0.57
1:S:918:GLU:HA	1:S:921:LYS:HD2	1.87	0.57
1:S:1312:ASP:HB2	1:S:1316:GLY:HA3	1.85	0.57
10:U:593:ARG:HD3	11:V:182:TRP:CZ3	2.40	0.57
11:V:1265:LEU:HD22	11:V:1323:ASP:HB3	1.86	0.57
1:A:310:VAL:HG13	1:A:311:ILE:HG13	1.86	0.57
6:G:474:SER:O	6:G:477:SER:OG	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:750:GLY:HA2	8:Q:556:LEU:HD12	1.86	0.57
6:H:70:GLU:O	6:H:74:THR:HG22	2.04	0.56
7:M:84:MET:HB3	7:M:88:LYS:NZ	2.19	0.56
2:O:181:MET:HB3	2:O:217:LEU:HD23	1.85	0.56
8:Q:549:THR:HA	8:Q:596:VAL:HG12	1.86	0.56
10:U:202:PHE:CE1	10:U:210:ILE:HG23	2.40	0.56
10:U:1248:LYS:HG3	10:U:1252:ASN:HD21	1.70	0.56
1:A:335:LYS:HE2	1:A:383:GLU:HB2	1.87	0.56
7:M:104:LEU:HD12	7:M:105:PRO:HD2	1.86	0.56
8:P:850:ARG:HH11	8:P:856:GLU:HB2	1.70	0.56
8:Q:464:ASN:O	8:Q:467:GLU:HG3	2.05	0.56
1:S:141:GLN:O	1:S:145:LEU:HG	2.06	0.56
1:A:198:GLU:OE2	1:A:262:MET:N	2.39	0.56
1:A:981:CYS:HA	1:A:984:LEU:HD12	1.86	0.56
2:B:777:ILE:HD12	2:B:830:VAL:HG11	1.86	0.56
4:E:388:THR:O	4:E:426:MET:HE3	2.05	0.56
6:H:606:ASP:HA	6:H:609:LEU:HG	1.87	0.56
8:Q:21:LEU:HB2	8:Q:399:LEU:HD21	1.88	0.56
8:Q:28:VAL:CG2	8:Q:37:LEU:HD13	2.36	0.56
8:Q:143:LEU:HD12	8:Q:197:LEU:HD21	1.87	0.56
1:S:346:TRP:CZ2	1:S:387:GLN:HG2	2.39	0.56
1:S:1257:LEU:HD12	1:S:1260:LEU:HD11	1.87	0.56
1:S:1302:TRP:CH2	1:S:1348:ILE:HD13	2.40	0.56
10:U:735:ILE:O	10:U:739:ASN:ND2	2.33	0.56
8:P:424:SER:O	8:P:424:SER:OG	2.23	0.56
8:Q:529:LEU:HD22	8:Q:572:LEU:HD11	1.87	0.56
1:S:603:PHE:O	1:S:607:LEU:HG	2.05	0.56
1:S:1045:GLU:HA	1:S:1104:ARG:HG2	1.86	0.56
10:U:494:GLN:OE1	10:U:498:ARG:NH2	2.32	0.56
1:A:1155:ILE:HA	1:A:1158:LYS:HZ3	1.69	0.56
1:A:1268:LEU:HA	1:A:1284:ALA:HB1	1.87	0.56
2:B:279:LEU:HD23	2:B:303:PHE:CZ	2.40	0.56
3:C:157:LEU:CD1	5:F:146:LEU:HD12	2.35	0.56
6:G:19:LYS:HE2	6:G:23:LEU:HD11	1.87	0.56
6:G:257:ARG:NE	6:G:285:GLU:OE2	2.31	0.56
8:Q:758:ALA:HB3	8:Q:761:GLY:H	1.71	0.56
1:S:288:GLU:HG3	1:S:292:HIS:CG	2.41	0.56
10:U:635:TYR:OH	10:U:712:ARG:NH1	2.39	0.56
1:A:285:VAL:HG23	1:A:287:GLU:OE1	2.06	0.56
2:B:231:PRO:O	2:B:234:SER:OG	2.24	0.56
2:B:814:LYS:O	2:B:818:ARG:HD2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:126:ARG:O	5:F:147:ARG:NH2	2.39	0.56
7:M:271:ILE:HG12	10:U:472:LEU:HD21	1.87	0.56
2:O:601:ILE:HG22	2:O:611:LYS:NZ	2.20	0.56
8:Q:479:ARG:HE	8:Q:610:VAL:HG11	1.71	0.56
10:U:82:GLN:H	10:U:85:ILE:HD11	1.70	0.56
11:V:265:LEU:O	11:V:269:LYS:NZ	2.31	0.56
11:V:832:VAL:HG12	11:V:833:THR:HG23	1.86	0.56
3:C:501:GLY:O	3:C:502:HIS:ND1	2.39	0.56
6:H:46:ALA:O	6:H:50:LEU:HG	2.05	0.56
7:L:342:LEU:HD22	7:L:357:GLY:HA3	1.87	0.56
2:O:509:LEU:HB2	2:O:596:THR:OG1	2.05	0.56
8:P:875:HIS:HB3	8:P:876:PRO:HD3	1.88	0.56
11:V:745:HIS:HB3	11:V:748:ASN:HB2	1.88	0.56
11:V:1092:HIS:HE1	11:V:1103:HIS:HA	1.71	0.56
5:F:156:ASN:HB3	5:F:158:GLN:NE2	2.20	0.56
2:O:338:THR:O	2:O:340:GLN:NE2	2.38	0.56
8:Q:253:VAL:HB	8:Q:272:VAL:HG23	1.87	0.56
8:Q:673:ARG:O	8:Q:674:ASP:HB2	2.05	0.56
1:S:1239:GLU:HA	1:S:1242:ILE:HD12	1.87	0.56
10:U:506:LEU:HB3	10:U:513:MET:CE	2.36	0.56
6:G:198:GLN:HE22	6:G:203:LEU:HD11	1.69	0.56
2:O:228:ILE:HG22	2:O:229:ILE:H	1.71	0.56
2:O:323:GLU:OE1	2:O:323:GLU:N	2.39	0.56
10:U:543:LEU:HB3	10:U:550:LEU:HD21	1.88	0.56
10:U:642:LEU:HG	10:U:716:SER:HA	1.87	0.56
1:A:60:LEU:HG	6:H:263:GLN:HB3	1.88	0.56
1:A:877:SER:O	1:A:881:GLN:HG2	2.06	0.56
1:A:1292:LEU:HD11	1:A:1342:PHE:HB2	1.88	0.56
6:G:219:GLU:HG2	6:G:224:ASN:HB2	1.87	0.56
8:P:84:GLY:HA3	8:P:126:PRO:HA	1.88	0.56
8:P:510:THR:HA	8:P:526:THR:O	2.06	0.56
1:S:656:ALA:HB1	1:S:680:ILE:HG12	1.88	0.56
1:A:792:GLY:HA2	1:A:814:VAL:HG21	1.89	0.55
6:H:90:GLU:CD	6:H:90:GLU:H	2.08	0.55
8:P:173:VAL:HG12	8:P:174:GLU:H	1.71	0.55
10:U:826:GLN:HE22	10:U:833:ARG:HH12	1.54	0.55
11:V:542:SER:HB2	11:V:545:ASN:ND2	2.21	0.55
1:A:361:ARG:O	1:A:365:MET:HG2	2.05	0.55
2:B:523:CYS:SG	2:B:582:THR:OG1	2.40	0.55
8:P:50:GLU:OE1	8:P:50:GLU:N	2.39	0.55
8:P:734:GLN:HE22	8:P:747:ARG:HB2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:688:LEU:HD21	1:A:757:VAL:HG22	1.88	0.55
2:B:284:PRO:HA	2:B:303:PHE:HD1	1.70	0.55
7:M:206:GLU:HG2	7:M:281:LEU:HD12	1.88	0.55
11:V:1251:PRO:HA	11:V:1312:LEU:HD21	1.88	0.55
1:A:244:LEU:HD23	1:A:248:GLN:HE22	1.70	0.55
1:A:403:ALA:HB1	1:A:406:LEU:HD11	1.89	0.55
1:S:393:VAL:HG12	1:S:396:LEU:HD12	1.89	0.55
1:S:481:VAL:HB	1:S:517:ARG:HD3	1.88	0.55
1:A:491:VAL:HA	1:A:494:LEU:HD12	1.87	0.55
3:C:281:LEU:N	3:C:282:PRO:HD2	2.22	0.55
6:G:479:CYS:O	6:G:483:LEU:HD13	2.07	0.55
2:O:691:VAL:HG12	2:O:706:THR:HG22	1.88	0.55
8:P:390:LEU:N	8:P:390:LEU:HD23	2.22	0.55
8:P:728:LEU:HB2	8:P:770:GLU:OE2	2.06	0.55
8:P:735:TRP:O	8:P:807:ARG:NH2	2.39	0.55
8:Q:715:LEU:O	8:Q:719:LEU:HB2	2.06	0.55
1:S:1186:ARG:O	1:S:1190:GLN:NE2	2.34	0.55
1:S:1363:LYS:O	1:S:1367:LEU:HG	2.07	0.55
11:V:565:SER:O	11:V:571:LYS:NZ	2.34	0.55
11:V:1261:HIS:HA	11:V:1264:LYS:HE2	1.88	0.55
2:O:526:ARG:HD3	8:Q:559:ALA:HA	1.89	0.55
10:U:595:LEU:O	10:U:602:ARG:NE	2.39	0.55
10:U:1052:ASP:HB3	10:U:1075:VAL:HG11	1.88	0.55
1:A:666:ASP:HB3	1:A:669:GLN:HE21	1.70	0.55
1:A:795:ARG:HH12	1:A:858:SER:C	2.09	0.55
1:A:946:LEU:HD13	1:A:950:GLU:HB3	1.88	0.55
6:G:151:LEU:HD11	6:G:211:PHE:HB2	1.88	0.55
7:L:44:GLU:OE1	7:L:44:GLU:N	2.39	0.55
8:Q:35:VAL:HG22	8:Q:47:TYR:O	2.06	0.55
10:U:823:GLN:HA	10:U:826:GLN:HB2	1.89	0.55
11:V:526:PRO:HB2	11:V:848:LEU:HD22	1.87	0.55
11:V:1307:LYS:HG3	11:V:1308:GLN:HG2	1.88	0.55
2:B:132:ASP:O	2:B:134:LEU:N	2.40	0.55
6:H:555:LEU:HD21	6:H:570:LEU:HB2	1.89	0.55
8:P:781:PRO:HG2	8:P:783:GLN:H	1.72	0.55
8:Q:733:LEU:HD11	8:Q:754:ILE:HG12	1.89	0.55
10:U:84:GLU:O	10:U:87:SER:OG	2.23	0.55
10:U:98:HIS:O	10:U:140:LYS:NZ	2.37	0.55
10:U:298:GLN:HG2	10:U:299:GLY:N	2.22	0.55
2:B:139:GLY:O	2:B:141:LEU:HB2	2.06	0.55
2:B:690:GLU:HG2	2:B:691:VAL:HG23	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:195:LEU:HD12	6:G:196:THR:H	1.71	0.55
8:Q:74:ARG:HG3	8:Q:90:LEU:HB2	1.89	0.55
1:S:184:HIS:HA	1:S:187:VAL:HG22	1.88	0.55
1:S:284:GLY:O	1:S:286:GLN:NE2	2.39	0.55
1:S:514:ALA:HA	1:S:517:ARG:HD2	1.89	0.55
1:S:931:ASP:O	1:S:935:LEU:HG	2.06	0.55
1:S:1080:ARG:NH2	1:S:1080:ARG:HA	2.21	0.55
1:S:1360:MET:HA	1:S:1363:LYS:HE2	1.89	0.55
11:V:1092:HIS:CE1	11:V:1103:HIS:HA	2.42	0.55
1:A:126:THR:HG23	1:A:176:SER:OG	2.07	0.55
3:C:213:GLU:OE1	3:C:220:PHE:CZ	2.60	0.55
6:G:256:HIS:HA	6:G:259:MET:HG2	1.89	0.55
6:G:374:LEU:HD13	6:G:393:MET:CE	2.37	0.55
6:H:548:ARG:HH21	6:H:609:LEU:HD21	1.71	0.55
7:M:107:PRO:HG2	7:M:108:PRO:CD	2.31	0.55
8:P:28:VAL:HG23	8:P:400:ASN:HD21	1.72	0.55
1:S:335:LYS:HE2	1:S:383:GLU:HB3	1.88	0.55
1:S:673:ILE:O	1:S:677:VAL:HG23	2.07	0.55
1:S:1052:PHE:O	1:S:1056:LEU:HG	2.06	0.55
1:S:1151:MET:O	1:S:1155:ILE:HG12	2.07	0.55
10:U:537:VAL:HG21	10:U:601:VAL:HG13	1.89	0.55
6:G:406:GLN:HG2	6:G:599:TRP:CE3	2.42	0.54
7:L:216:PRO:HG2	7:L:226:ARG:HD3	1.87	0.54
2:O:140:PRO:HG2	2:O:155:SER:HB3	1.90	0.54
2:O:520:LEU:HG	2:O:521:LEU:H	1.73	0.54
2:O:854:GLN:O	2:O:858:ASN:ND2	2.40	0.54
8:P:767:ILE:CG1	8:P:788:GLN:HB3	2.36	0.54
1:S:752:THR:OG1	1:S:753:MET:SD	2.65	0.54
1:S:1094:SER:HA	1:S:1145:SER:HB3	1.89	0.54
10:U:234:ILE:HD13	10:U:293:LEU:HD21	1.89	0.54
6:G:79:ILE:HG13	6:G:145:LEU:HD21	1.89	0.54
2:O:73:HIS:HB3	2:O:99:ASN:HB3	1.89	0.54
11:V:101:GLU:HA	11:V:104:ILE:HG12	1.88	0.54
11:V:186:VAL:O	11:V:186:VAL:HG23	2.07	0.54
11:V:514:VAL:O	11:V:517:ILE:HG22	2.07	0.54
11:V:1025:ASN:HD22	11:V:1097:ARG:HD3	1.72	0.54
1:A:1261:PHE:O	1:A:1265:LEU:HG	2.06	0.54
5:F:129:LEU:O	5:F:132:SER:OG	2.24	0.54
7:M:212:TRP:NE1	7:M:298:LEU:HB2	2.22	0.54
1:S:155:LEU:HA	1:S:160:MET:HE2	1.89	0.54
1:S:504:ARG:HE	1:S:507:LEU:HD12	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:1018:ILE:HG12	1:S:1084:ARG:HD2	1.89	0.54
10:U:1029:MET:HG3	10:U:1087:LEU:HD22	1.88	0.54
10:U:1167:CYS:O	10:U:1171:THR:HG23	2.07	0.54
11:V:173:PRO:HA	11:V:176:ILE:HG22	1.89	0.54
11:V:1115:VAL:HG21	11:V:1142:LEU:HG	1.90	0.54
11:V:1306:LEU:HD21	11:V:1367:LEU:HB3	1.89	0.54
2:B:619:ARG:HH12	8:P:635:GLN:HB3	1.72	0.54
3:C:127:PHE:HE1	5:F:147:ARG:HD3	1.72	0.54
7:L:351:SER:OG	7:L:354:ILE:HB	2.07	0.54
2:O:186:LEU:HB3	2:O:212:PHE:CD1	2.43	0.54
2:O:765:LYS:HZ1	2:O:848:LYS:HB2	1.72	0.54
8:P:41:SER:OG	8:P:42:GLU:N	2.41	0.54
8:Q:807:ARG:O	8:Q:810:THR:OG1	2.24	0.54
10:U:85:ILE:O	10:U:89:ILE:HG12	2.08	0.54
11:V:278:LEU:HA	11:V:281:ILE:HD12	1.90	0.54
1:A:179:LEU:HD23	1:A:217:LEU:HD11	1.90	0.54
2:B:122:LEU:HD21	2:B:155:SER:HA	1.90	0.54
2:B:426:LEU:O	2:B:429:LEU:HG	2.07	0.54
3:C:137:GLY:O	5:F:195:ARG:NH2	2.40	0.54
7:L:320:PRO:HA	7:L:333:PHE:O	2.07	0.54
10:U:134:LEU:HB3	10:U:157:LYS:HG3	1.89	0.54
11:V:383:VAL:HG21	11:V:424:HIS:CD2	2.43	0.54
2:B:423:TYR:CE1	8:P:606:LEU:HB3	2.41	0.54
4:E:290:ARG:NH2	4:E:312:GLU:OE2	2.41	0.54
8:P:177:SER:OG	8:P:249:GLN:NE2	2.41	0.54
8:P:815:GLN:O	8:P:818:GLN:NE2	2.40	0.54
1:S:1415:PHE:HB3	1:S:1440:GLN:HG2	1.89	0.54
11:V:273:ILE:HG22	11:V:274:ARG:O	2.07	0.54
11:V:371:THR:O	11:V:377:HIS:HE1	1.91	0.54
11:V:1111:LEU:HD11	11:V:1144:LYS:HE2	1.88	0.54
1:A:779:PRO:HA	1:A:782:LEU:HG	1.90	0.54
1:A:932:TRP:CZ3	1:A:936:GLU:HG2	2.42	0.54
8:Q:585:GLY:O	8:Q:587:GLY:N	2.41	0.54
1:S:934:HIS:HA	1:S:937:LEU:HD12	1.87	0.54
1:A:653:LEU:HD11	1:A:687:VAL:HG11	1.89	0.54
4:E:438:LEU:HD11	4:E:462:VAL:HG11	1.88	0.54
6:H:63:ALA:O	6:H:66:VAL:HG12	2.07	0.54
2:O:855:LYS:HA	2:O:858:ASN:HD21	1.73	0.54
3:C:408:ALA:HB3	3:C:493:ASN:HD22	1.73	0.54
2:O:767:LEU:HD13	8:Q:841:LEU:HA	1.90	0.54
11:V:59:LEU:HD13	11:V:66:ASN:HD21	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Q:76:LEU:HG	8:Q:90:LEU:HD21	1.88	0.54
8:Q:767:ILE:CG1	8:Q:788:GLN:HB3	2.36	0.54
1:S:764:ARG:HH21	1:S:768:LEU:HD23	1.73	0.54
11:V:243:VAL:HG13	11:V:244:PRO:HD3	1.89	0.54
1:A:31:LYS:NZ	6:H:377:SER:OG	2.34	0.53
1:A:1112:VAL:HA	1:A:1116:MET:HG2	1.88	0.53
1:A:1178:GLU:CG	1:A:1179:PRO:HD3	2.38	0.53
6:G:62:ALA:HB2	6:G:102:ARG:HD2	1.90	0.53
2:O:585:SER:OG	2:O:586:PRO:HD3	2.08	0.53
8:P:366:LEU:HD23	8:P:366:LEU:C	2.28	0.53
8:P:526:THR:HG22	8:P:581:THR:HG22	1.90	0.53
1:S:171:TRP:CE3	1:S:200:HIS:HD2	2.26	0.53
1:S:555:ILE:HG21	1:S:1007:VAL:HG11	1.89	0.53
1:S:739:PRO:HD3	1:S:898:LEU:HD11	1.90	0.53
1:S:769:LEU:HG	1:S:821:LEU:HD11	1.90	0.53
11:V:282:ILE:HA	11:V:285:ILE:HD12	1.89	0.53
11:V:752:ILE:HG13	11:V:755:LEU:HB2	1.90	0.53
1:A:1165:LEU:HD11	1:A:1321:ARG:O	2.07	0.53
5:F:246:GLU:N	5:F:246:GLU:OE1	2.40	0.53
8:P:51:GLY:O	8:P:53:LEU:N	2.38	0.53
1:S:171:TRP:HZ2	1:S:197:LEU:HA	1.74	0.53
10:U:1036:HIS:CE1	10:U:1042:PRO:HA	2.43	0.53
10:U:1277:GLN:HE22	10:U:1278:HIS:CD2	2.26	0.53
11:V:532:LEU:HD23	11:V:536:LEU:HD13	1.89	0.53
1:A:191:VAL:HG12	1:A:192:SER:H	1.72	0.53
1:A:232:ARG:HA	1:A:235:LEU:HG	1.91	0.53
1:A:288:GLU:OE2	1:A:288:GLU:N	2.38	0.53
2:B:143:LEU:HD11	2:B:183:LEU:HD21	1.89	0.53
3:C:430:TYR:O	4:E:176:ARG:HG3	2.09	0.53
5:F:35:LEU:HD23	5:F:90:ASP:OD1	2.09	0.53
6:G:89:THR:HG21	8:P:147:PRO:HB3	1.91	0.53
10:U:708:SER:HG	10:U:712:ARG:HH11	1.54	0.53
2:B:635:THR:O	2:B:639:LYS:HB2	2.08	0.53
3:C:66:THR:HG22	3:C:69:GLN:HB2	1.89	0.53
2:O:762:THR:HB	2:O:849:SER:HA	1.91	0.53
8:P:529:LEU:HD12	8:P:543:LEU:HD22	1.90	0.53
8:Q:806:GLY:O	8:Q:810:THR:HG23	2.08	0.53
10:U:785:LEU:HB3	10:U:799:LYS:HD3	1.89	0.53
10:U:827:GLU:OE1	10:U:827:GLU:N	2.42	0.53
2:B:90:ASN:O	2:B:91:LEU:HG	2.09	0.53
4:E:156:LEU:HB3	4:E:160:CYS:SG	2.48	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:57:LEU:HD11	1:S:101:GLN:HG3	1.91	0.53
11:V:624:SER:HB3	11:V:627:ALA:HB3	1.91	0.53
1:A:1422:LEU:HD21	1:A:1433:SER:HB3	1.89	0.53
3:C:64:PHE:N	3:C:65:PRO:HD2	2.24	0.53
4:E:487:MET:N	4:E:487:MET:SD	2.82	0.53
6:G:267:LEU:HB3	1:S:93:PHE:CE2	2.44	0.53
6:H:176:ASP:OD1	6:H:178:LEU:N	2.42	0.53
7:M:151:THR:HB	7:M:166:PHE:HB2	1.90	0.53
8:P:328:TRP:HA	8:P:333:LYS:O	2.08	0.53
11:V:255:ASP:OD1	11:V:255:ASP:N	2.41	0.53
1:A:399:CYS:SG	1:A:400:PHE:N	2.81	0.53
3:C:245:ARG:HA	4:E:96:ARG:NH1	2.24	0.53
4:E:360:ALA:O	4:E:364:THR:HG23	2.09	0.53
5:F:9:ASP:OD1	5:F:10:ARG:N	2.41	0.53
5:F:111:LEU:HG	5:F:115:LEU:HD11	1.91	0.53
7:M:214:LEU:HD12	7:M:229:ALA:HB2	1.90	0.53
8:Q:227:LEU:HD13	8:Q:334:LEU:HB3	1.90	0.53
1:S:1311:SER:HA	1:S:1317:ARG:HD2	1.90	0.53
10:U:549:VAL:HG23	10:U:580:ASN:ND2	2.23	0.53
10:U:602:ARG:NH1	10:U:662:GLU:HB2	2.23	0.53
1:A:460:ARG:NH2	1:A:497:PRO:O	2.42	0.53
2:B:54:THR:OG1	2:B:56:VAL:HG22	2.08	0.53
2:B:65:PHE:CD1	2:B:118:PHE:HB2	2.44	0.53
3:C:364:TRP:HH2	3:C:538:ILE:HG13	1.72	0.53
6:H:461:GLN:NE2	6:H:465:GLN:HE21	2.06	0.53
8:P:459:LEU:HA	8:P:462:ILE:HD12	1.91	0.53
8:Q:360:HIS:CE1	8:Q:367:CYS:HB2	2.44	0.53
1:S:607:LEU:HB3	1:S:613:ILE:HD11	1.90	0.53
10:U:298:GLN:HG2	10:U:299:GLY:H	1.73	0.53
10:U:832:LEU:HB3	10:U:838:PHE:HE2	1.72	0.53
10:U:931:LEU:HD23	10:U:934:LEU:HD12	1.91	0.53
11:V:976:LEU:HD21	11:V:1016:VAL:HG11	1.89	0.53
1:A:657:LEU:HD22	1:A:725:SER:HB2	1.91	0.53
1:A:1126:LEU:HD11	1:A:1165:LEU:HB3	1.91	0.53
6:H:102:ARG:O	6:H:105:GLU:HG2	2.09	0.53
1:S:727:CYS:SG	9:W:87:TRP:NE1	2.76	0.53
1:S:788:ALA:HB1	1:S:818:PHE:HE1	1.73	0.53
4:E:298:LEU:HD21	4:E:347:TRP:CH2	2.43	0.53
2:O:89:ILE:O	2:O:91:LEU:HD12	2.09	0.53
8:P:227:LEU:HB2	8:P:334:LEU:HD21	1.91	0.53
8:Q:328:TRP:HA	8:Q:333:LYS:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:915:THR:O	1:S:919:VAL:HG23	2.09	0.53
1:S:1087:SER:OG	1:S:1133:HIS:O	2.18	0.53
10:U:447:ARG:HG2	10:U:451:ARG:HG21	1.73	0.53
3:C:339:THR:HG22	3:C:339:THR:O	2.09	0.52
2:O:603:GLU:HG3	2:O:611:LYS:HE2	1.90	0.52
2:O:675:TRP:CZ3	2:O:734:LEU:HD12	2.43	0.52
8:Q:796:ASP:OD1	8:Q:799:ARG:NH1	2.42	0.52
1:S:278:LEU:HD11	1:S:327:ILE:HA	1.90	0.52
2:B:357:PHE:CD1	2:B:357:PHE:C	2.82	0.52
4:E:22:LEU:O	4:E:27:ARG:NH2	2.42	0.52
4:E:156:LEU:HB3	4:E:160:CYS:HG	1.74	0.52
7:L:307:CYS:HB3	7:L:310:CYS:SG	2.48	0.52
7:M:123:TRP:HB3	2:O:386:ASN:HB3	1.91	0.52
2:O:385:GLU:O	2:O:389:LEU:HB2	2.09	0.52
1:S:801:VAL:HG22	9:W:6:UNK:HA	1.91	0.52
10:U:889:PRO:HG2	10:U:892:VAL:HG13	1.90	0.52
10:U:1028:LEU:O	10:U:1032:LEU:HG	2.09	0.52
1:A:1053:ARG:O	1:A:1057:GLN:HG3	2.09	0.52
2:B:31:ASN:O	2:B:39:LYS:N	2.37	0.52
6:G:89:THR:HG22	6:G:90:GLU:H	1.73	0.52
6:H:117:GLY:O	6:H:121:LEU:HD23	2.09	0.52
6:H:242:ARG:O	6:H:246:VAL:HG23	2.09	0.52
7:M:201:TRP:CH2	7:M:221:ARG:HB3	2.43	0.52
8:P:77:TYR:HE1	8:P:87:CYS:HG	1.57	0.52
1:S:372:VAL:HA	1:S:375:LEU:HD12	1.91	0.52
1:S:1003:ASN:OD1	9:W:1:UNK:N	2.39	0.52
1:A:404:GLN:O	1:A:407:LEU:HG	2.09	0.52
2:B:777:ILE:HD12	2:B:830:VAL:CG1	2.39	0.52
7:M:104:LEU:CD1	7:M:105:PRO:HD2	2.40	0.52
7:M:170:PRO:HD2	7:M:197:LEU:HD21	1.92	0.52
8:P:202:PRO:HB3	8:P:225:PHE:CE2	2.44	0.52
1:S:91:SER:OG	1:S:92:SER:N	2.42	0.52
1:S:928:THR:HB	1:S:971:GLY:HA3	1.92	0.52
1:A:1415:PHE:CZ	1:A:1439:ARG:HG2	2.44	0.52
6:G:58:GLN:HE22	6:G:98:ARG:HG2	1.75	0.52
6:H:337:PRO:HG2	6:H:338:LEU:HD22	1.91	0.52
7:M:349:ARG:NH1	10:U:374:SER:O	2.42	0.52
1:S:288:GLU:OE1	1:S:288:GLU:N	2.40	0.52
1:S:787:LEU:O	1:S:791:LEU:HG	2.10	0.52
1:A:831:PHE:O	1:A:834:LEU:HG	2.10	0.52
1:A:985:VAL:O	1:A:989:MET:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:423:TYR:CD1	8:P:606:LEU:HD13	2.44	0.52
4:E:359:ASN:HD21	7:M:73:ARG:HH12	1.57	0.52
8:P:150:TRP:HZ3	8:P:195:PRO:HG3	1.73	0.52
1:S:746:ALA:O	1:S:750:VAL:HG23	2.08	0.52
10:U:757:ASN:HA	10:U:760:ILE:HD12	1.90	0.52
11:V:933:PHE:CE2	11:V:972:LEU:HD13	2.45	0.52
4:E:310:PRO:HB2	4:E:312:GLU:OE1	2.10	0.52
2:O:78:CYS:HB2	2:O:95:VAL:HB	1.92	0.52
1:S:314:ASP:HB2	1:S:315:PRO:HD3	1.91	0.52
11:V:1350:ASP:HB3	11:V:1353:LEU:HB2	1.90	0.52
1:A:649:PRO:HB2	1:A:687:VAL:HG12	1.92	0.52
1:A:656:ALA:HA	1:A:659:GLU:HB3	1.92	0.52
1:A:956:GLN:OE1	1:A:1020:ARG:NH1	2.43	0.52
1:A:1080:ARG:NH2	1:S:952:GLN:HB2	2.24	0.52
1:A:1178:GLU:HG3	1:A:1179:PRO:HD3	1.91	0.52
6:G:327:LEU:HD12	6:G:327:LEU:H	1.75	0.52
8:P:165:ARG:HG3	8:P:166:PRO:HD2	1.91	0.52
1:S:399:CYS:O	1:S:670:ARG:NH1	2.42	0.52
10:U:671:ILE:HG23	10:U:702:LEU:HD11	1.92	0.52
11:V:243:VAL:CG1	11:V:244:PRO:HD3	2.40	0.52
11:V:268:ASP:O	11:V:304:LYS:NZ	2.42	0.52
11:V:830:LEU:HD12	11:V:916:LEU:HB3	1.92	0.52
11:V:1082:GLU:OE2	11:V:1082:GLU:N	2.39	0.52
11:V:1135:ILE:HD11	11:V:1155:ILE:HG23	1.92	0.52
1:A:64:VAL:HG23	1:A:65:GLU:H	1.75	0.52
2:B:40:THR:OG1	2:B:41:PRO:HD2	2.10	0.52
2:O:520:LEU:HD12	8:Q:567:ILE:CG1	2.38	0.52
8:P:712:ALA:H	8:P:782:ILE:HG21	1.74	0.52
8:Q:729:CYS:HB3	8:Q:752:SER:OG	2.10	0.52
11:V:372:ALA:HA	11:V:406:LYS:NZ	2.24	0.52
11:V:613:LEU:O	11:V:617:VAL:HG23	2.10	0.52
1:A:1231:HIS:O	1:A:1235:GLN:HG3	2.09	0.52
2:B:25:PHE:CD2	2:B:94:ILE:HD11	2.44	0.52
3:C:127:PHE:CZ	5:F:162:LEU:HD11	2.45	0.52
4:E:160:CYS:SG	4:E:161:GLN:N	2.83	0.52
6:G:453:SER:OG	6:G:454:ALA:N	2.42	0.52
7:M:277:GLU:OE1	7:M:277:GLU:N	2.41	0.52
2:O:111:ILE:HD12	2:O:121:ARG:HG3	1.92	0.52
8:P:545:ILE:HD11	8:P:565:TYR:HB2	1.92	0.52
1:S:1019:SER:O	1:S:1022:GLN:HB2	2.10	0.52
10:U:66:ARG:NH2	10:U:111:GLU:OE2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:LEU:O	1:A:417:GLN:HG3	2.10	0.51
1:A:1412:LYS:HD2	1:A:1443:ALA:HB2	1.90	0.51
2:B:195:GLU:O	2:B:195:GLU:HG2	2.09	0.51
2:B:423:TYR:CD1	8:P:606:LEU:HD22	2.45	0.51
4:E:333:LEU:HA	4:E:336:LEU:HD23	1.92	0.51
2:O:707:TRP:CH2	2:O:715:GLY:HA3	2.44	0.51
2:O:774:SER:OG	8:Q:834:HIS:HB2	2.11	0.51
8:P:165:ARG:HE	8:P:166:PRO:HD2	1.71	0.51
8:P:173:VAL:HG12	8:P:174:GLU:N	2.25	0.51
8:Q:31:HIS:O	8:Q:33:ALA:N	2.37	0.51
8:Q:526:THR:HG22	8:Q:581:THR:HG22	1.92	0.51
10:U:840:ARG:O	10:U:844:ASN:ND2	2.39	0.51
10:U:1173:LEU:HA	10:U:1176:LEU:HD12	1.92	0.51
1:A:102:ALA:HB2	1:A:112:LEU:HD12	1.93	0.51
1:A:827:ARG:HH21	1:A:944:ASP:N	2.08	0.51
3:C:241:CYS:SG	4:E:37:PRO:HD2	2.48	0.51
8:Q:739:GLU:N	8:Q:739:GLU:OE1	2.40	0.51
10:U:332:THR:O	10:U:336:LYS:HG2	2.10	0.51
11:V:154:PHE:CZ	11:V:196:ILE:HG22	2.46	0.51
1:A:1134:PHE:CE2	1:A:1138:LEU:HD11	2.45	0.51
3:C:457:SER:HB3	3:C:494:PHE:HE1	1.76	0.51
6:H:565:ASP:OD1	6:H:565:ASP:N	2.43	0.51
7:M:215:GLU:CD	7:M:319:ILE:HD11	2.31	0.51
1:S:1148:PRO:O	1:S:1152:VAL:HG23	2.10	0.51
10:U:1076:ASN:HB2	10:U:1079:THR:HG23	1.92	0.51
11:V:78:LYS:HD2	11:V:81:GLN:HE21	1.75	0.51
11:V:456:LEU:HD12	11:V:460:TYR:CE2	2.45	0.51
11:V:1370:ARG:O	11:V:1374:MET:HG2	2.10	0.51
1:A:1193:LEU:O	1:A:1198:GLN:NE2	2.43	0.51
2:B:347:ASP:OD1	2:B:347:ASP:N	2.43	0.51
4:E:408:GLN:HE21	4:E:444:LEU:HD22	1.76	0.51
6:G:241:PRO:O	6:G:244:VAL:HG12	2.10	0.51
7:M:107:PRO:CD	7:M:108:PRO:HD2	2.40	0.51
2:O:711:THR:O	2:O:713:PHE:N	2.44	0.51
8:P:801:HIS:O	8:P:805:VAL:HG22	2.09	0.51
1:S:512:SER:O	1:S:516:THR:HG23	2.10	0.51
10:U:1:MET:HA	10:U:4:LYS:NZ	2.26	0.51
11:V:362:GLU:O	11:V:366:LYS:HG3	2.10	0.51
11:V:620:CYS:O	11:V:623:GLN:OE1	2.28	0.51
2:B:187:LYS:HG2	2:B:229:ILE:HD11	1.91	0.51
3:C:19:LEU:HD12	3:C:70:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:361:ARG:HD2	3:C:538:ILE:HD12	1.92	0.51
6:G:270:VAL:HG23	1:S:48:VAL:HG23	1.91	0.51
8:P:505:PRO:HA	8:P:533:SER:HB2	1.93	0.51
8:P:866:LEU:HA	8:P:869:VAL:HG22	1.93	0.51
1:S:291:THR:HA	1:S:294:ILE:HD12	1.91	0.51
1:S:717:MET:O	1:S:721:LEU:HG	2.10	0.51
1:S:984:LEU:HD22	1:S:1021:LEU:HD13	1.91	0.51
10:U:642:LEU:HD11	10:U:715:LYS:HG3	1.93	0.51
10:U:987:THR:O	10:U:990:THR:OG1	2.24	0.51
11:V:582:ALA:HB1	11:V:610:VAL:HG23	1.93	0.51
11:V:843:PHE:CD2	11:V:847:THR:HG21	2.46	0.51
11:V:1111:LEU:HD21	11:V:1144:LYS:HB2	1.93	0.51
2:B:506:LEU:H	2:B:525:ASN:ND2	2.05	0.51
3:C:123:SER:O	3:C:123:SER:OG	2.28	0.51
2:O:18:TYR:OH	2:O:90:ASN:O	2.15	0.51
8:P:125:LEU:HD23	8:P:166:PRO:HB3	1.93	0.51
8:Q:33:ALA:HB1	8:Q:50:GLU:OE2	2.10	0.51
1:S:152:ALA:HA	1:S:155:LEU:HD12	1.91	0.51
1:S:1143:LEU:HB3	1:S:1188:HIS:CD2	2.45	0.51
10:U:54:SER:O	10:U:65:ARG:NH2	2.42	0.51
10:U:72:CYS:HA	10:U:75:LEU:HG	1.91	0.51
10:U:591:LEU:HD22	10:U:605:LEU:HD11	1.92	0.51
5:F:199:ASN:OD1	5:F:203:LYS:NZ	2.44	0.51
6:H:501:GLN:HA	6:H:504:LYS:HD3	1.91	0.51
2:O:636:PHE:HZ	2:O:651:LEU:HD21	1.74	0.51
1:S:759:PRO:O	1:S:763:THR:HG23	2.10	0.51
10:U:1006:MET:O	10:U:1010:THR:HG23	2.11	0.51
2:B:385:GLU:N	7:L:123:TRP:HB2	2.26	0.51
2:B:835:TYR:O	2:B:839:THR:HG23	2.10	0.51
3:C:87:GLN:HG2	3:C:88:LYS:N	2.26	0.51
3:C:213:GLU:OE1	3:C:220:PHE:HE2	1.93	0.51
3:C:213:GLU:HG3	3:C:215:LEU:O	2.10	0.51
4:E:400:SER:HA	4:E:440:GLN:NE2	2.25	0.51
2:O:83:SER:HA	2:O:89:ILE:O	2.11	0.51
8:P:249:GLN:HB3	8:P:277:HIS:HD2	1.76	0.51
8:Q:14:PHE:N	8:Q:427:GLY:O	2.31	0.51
10:U:648:GLU:OE1	10:U:648:GLU:N	2.39	0.51
11:V:442:LEU:HD22	11:V:450:ILE:HG23	1.93	0.51
1:A:22:TRP:HH2	6:H:375:LEU:HD13	1.76	0.51
2:O:141:LEU:HD11	2:O:152:PHE:HB2	1.91	0.51
8:Q:570:ASP:OD1	8:Q:578:ARG:NH1	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:424:LEU:O	1:S:428:VAL:HG23	2.11	0.51
10:U:368:VAL:O	10:U:371:SER:HB2	2.11	0.51
11:V:48:PHE:HA	11:V:96:PHE:CE1	2.46	0.51
1:A:713:PRO:O	1:A:717:MET:HG2	2.11	0.51
4:E:516:LEU:HD13	4:E:527:LEU:HB3	1.93	0.51
7:M:274:TRP:HE3	7:M:287:VAL:HG21	1.75	0.51
10:U:1135:ILE:HG13	10:U:1197:LEU:HD22	1.92	0.51
1:A:1310:GLU:O	1:A:1317:ARG:NH1	2.43	0.50
2:B:281:PHE:HB2	2:B:303:PHE:CE2	2.47	0.50
3:C:87:GLN:O	3:C:91:ILE:HG13	2.11	0.50
3:C:124:ALA:O	5:F:140:ARG:NH1	2.45	0.50
3:C:265:GLU:HG3	3:C:268:CYS:HB3	1.93	0.50
8:P:31:HIS:O	8:P:32:GLU:C	2.49	0.50
8:P:729:CYS:SG	8:P:752:SER:OG	2.56	0.50
8:P:733:LEU:HD22	8:P:746:VAL:HG11	1.92	0.50
1:S:572:SER:OG	1:S:612:LYS:NZ	2.44	0.50
11:V:364:TRP:HZ2	11:V:380:PHE:CE1	2.28	0.50
3:C:174:ARG:NE	3:C:209:ARG:NH1	2.60	0.50
7:M:107:PRO:CB	2:O:401:CYS:SG	2.99	0.50
1:S:650:LEU:O	1:S:654:THR:HG23	2.11	0.50
1:S:936:GLU:O	1:S:1014:ASN:ND2	2.39	0.50
1:S:1112:VAL:HA	1:S:1116:MET:HG2	1.93	0.50
10:U:50:ILE:O	10:U:54:SER:OG	2.26	0.50
10:U:465:ASN:O	10:U:468:MET:HG3	2.11	0.50
11:V:76:GLN:NE2	11:V:138:LEU:O	2.44	0.50
11:V:84:ARG:HA	11:V:89:TYR:HE1	1.75	0.50
11:V:1208:VAL:HG13	11:V:1209:PRO:HD3	1.94	0.50
1:A:179:LEU:HD23	1:A:217:LEU:CD1	2.42	0.50
1:A:1139:LEU:HD22	1:A:1184:ARG:HD3	1.92	0.50
1:A:1169:SER:O	1:A:1172:VAL:HG22	2.11	0.50
2:B:242:ILE:HG12	2:B:256:LEU:HD12	1.92	0.50
5:F:252:CYS:HB3	5:F:274:TYR:CE1	2.47	0.50
6:G:31:GLN:HE22	6:G:322:LEU:HB2	1.77	0.50
8:P:806:GLY:O	8:P:810:THR:HG23	2.12	0.50
1:S:377:GLU:O	1:S:381:THR:OG1	2.20	0.50
1:S:1108:PHE:O	1:S:1112:VAL:HG23	2.12	0.50
11:V:696:ALA:HA	11:V:758:CYS:SG	2.51	0.50
1:A:1025:VAL:O	1:A:1029:GLU:HG2	2.11	0.50
2:B:196:CYS:O	2:B:197:THR:OG1	2.25	0.50
3:C:212:GLN:HE21	3:C:212:GLN:CA	2.16	0.50
3:C:324:GLU:O	3:C:328:LYS:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:455:GLN:HE21	4:E:495:THR:HG21	1.76	0.50
8:P:340:GLU:N	8:P:340:GLU:OE2	2.45	0.50
8:P:773:MET:O	8:P:781:PRO:HB3	2.11	0.50
1:S:460:ARG:HA	1:S:463:HIS:CD2	2.46	0.50
1:S:1080:ARG:NH2	1:S:1083:LEU:HD12	2.26	0.50
10:U:51:PHE:O	10:U:65:ARG:NH2	2.44	0.50
10:U:497:GLN:HG2	10:U:538:ALA:HB1	1.94	0.50
6:H:29:VAL:O	6:H:33:SER:OG	2.27	0.50
8:Q:538:ASP:CG	8:Q:539:GLN:H	2.15	0.50
1:S:904:GLN:OE1	1:S:904:GLN:N	2.43	0.50
10:U:546:ASN:O	10:U:615:ARG:NH2	2.43	0.50
11:V:580:THR:O	11:V:584:ILE:HG12	2.12	0.50
1:A:23:ALA:HA	1:A:26:LEU:CD1	2.39	0.50
1:A:1019:SER:O	1:A:1023:GLU:HG3	2.12	0.50
1:A:1402:PHE:O	1:A:1406:LEU:HD23	2.12	0.50
8:Q:31:HIS:HB2	8:Q:69:LEU:HD11	1.93	0.50
8:Q:655:PHE:CZ	8:Q:754:ILE:HD12	2.46	0.50
10:U:488:LEU:HD12	10:U:491:LEU:HD12	1.94	0.50
11:V:394:GLN:N	11:V:394:GLN:OE1	2.42	0.50
1:A:417:GLN:NE2	1:A:426:SER:OG	2.45	0.50
2:B:693:PHE:HD2	2:B:704:LEU:HD21	1.76	0.50
3:C:127:PHE:HZ	5:F:162:LEU:HD11	1.76	0.50
5:F:15:LEU:O	5:F:18:SER:OG	2.21	0.50
6:G:367:TYR:OH	6:G:399:GLU:OE2	2.29	0.50
6:G:416:LEU:HD12	1:S:22:TRP:CZ3	2.41	0.50
2:O:74:LEU:HD21	2:O:98:LYS:HD3	1.93	0.50
2:O:661:GLN:HB2	2:O:747:LEU:HD11	1.93	0.50
8:Q:709:LYS:HB2	8:Q:879:ILE:HD12	1.92	0.50
1:S:932:TRP:HE3	1:S:933:LEU:HD23	1.77	0.50
10:U:470:ALA:O	10:U:473:VAL:HG12	2.12	0.50
11:V:165:LYS:NZ	11:V:169:GLU:OE1	2.33	0.50
1:A:1420:GLU:OE1	1:A:1420:GLU:N	2.43	0.50
7:M:89:MET:O	7:M:93:VAL:HG23	2.12	0.50
2:O:218:GLU:HB3	2:O:220:GLN:HE22	1.75	0.50
8:P:344:PRO:HD2	8:P:390:LEU:HD11	1.93	0.50
8:Q:47:TYR:CZ	8:Q:54:LEU:HB3	2.46	0.50
1:S:485:SER:O	1:S:490:GLN:NE2	2.45	0.50
11:V:1109:GLU:OE2	11:V:1113:GLN:NE2	2.44	0.50
11:V:1210:GLU:OE1	11:V:1210:GLU:N	2.44	0.50
1:A:664:MET:HE1	1:A:733:ALA:HB2	1.94	0.50
1:A:1329:ARG:HB3	1:A:1330:LEU:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:150:PHE:CZ	2:B:170:ILE:HB	2.46	0.50
6:G:23:LEU:HD23	6:G:50:LEU:HD12	1.93	0.50
7:L:267:LEU:O	7:L:271:ILE:HG23	2.12	0.50
2:O:635:THR:HG22	2:O:639:LYS:HE3	1.94	0.50
8:P:361:SER:CB	8:P:398:SER:O	2.59	0.50
1:S:764:ARG:O	1:S:768:LEU:HG	2.11	0.50
1:S:1113:ASN:O	1:S:1117:ARG:NE	2.40	0.50
11:V:234:LEU:HD22	11:V:245:ILE:HD11	1.92	0.50
11:V:526:PRO:HA	11:V:529:ILE:HD12	1.93	0.50
1:A:121:VAL:HA	1:A:124:ILE:HG22	1.93	0.49
2:B:479:TRP:HZ2	2:B:577:ILE:HD12	1.77	0.49
3:C:126:ARG:HH22	5:F:140:ARG:HG2	1.76	0.49
6:H:596:TYR:O	6:H:600:ILE:HD12	2.12	0.49
7:L:83:PHE:C	7:L:83:PHE:CD1	2.85	0.49
7:M:326:ASN:HD22	7:M:364:LYS:HG3	1.77	0.49
2:O:216:SER:CB	2:O:220:GLN:HB2	2.42	0.49
2:O:529:LYS:HG2	2:O:576:GLN:HG3	1.92	0.49
8:P:150:TRP:CE2	8:P:178:TYR:HE2	2.29	0.49
1:S:34:LYS:HB3	1:S:39:ARG:HH21	1.76	0.49
1:S:313:THR:HG23	1:S:316:LEU:HB3	1.92	0.49
1:S:788:ALA:HB1	1:S:818:PHE:CE1	2.46	0.49
10:U:654:GLN:O	10:U:657:LYS:NZ	2.44	0.49
10:U:1029:MET:HA	10:U:1032:LEU:HD12	1.94	0.49
11:V:1009:ALA:O	11:V:1013:VAL:HG23	2.11	0.49
11:V:1122:HIS:HB3	11:V:1158:LEU:HD11	1.94	0.49
2:B:281:PHE:HB2	2:B:303:PHE:CD2	2.48	0.49
5:F:111:LEU:O	5:F:115:LEU:HD12	2.11	0.49
6:G:541:VAL:HG21	6:G:554:LEU:HD22	1.94	0.49
6:H:558:LEU:O	6:H:562:ASP:N	2.41	0.49
8:P:200:VAL:O	8:P:200:VAL:CG1	2.61	0.49
8:P:864:GLN:OE1	8:P:871:ARG:NH2	2.45	0.49
8:Q:598:VAL:HG13	8:Q:645:HIS:HB3	1.94	0.49
1:S:307:LEU:O	1:S:311:ILE:HG22	2.12	0.49
9:W:77:VAL:HB	9:W:85:PHE:HD2	1.76	0.49
10:U:364:ILE:O	10:U:367:VAL:HB	2.13	0.49
10:U:579:ALA:HA	10:U:582:THR:HG22	1.94	0.49
11:V:928:LEU:O	11:V:975:LYS:NZ	2.40	0.49
2:B:526:ARG:NH2	2:B:655:PHE:O	2.40	0.49
3:C:23:ASP:OD2	3:C:24:GLN:HG3	2.12	0.49
3:C:142:PRO:HA	3:C:145:TYR:HE2	1.72	0.49
4:E:24:ALA:HA	4:E:27:ARG:NH2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:408:GLN:NE2	4:E:444:LEU:HD22	2.27	0.49
6:G:186:PRO:HD3	6:G:204:LYS:HD2	1.94	0.49
6:G:553:HIS:O	6:G:557:THR:HG23	2.12	0.49
7:L:54:LEU:HG	7:L:55:CYS:H	1.77	0.49
8:P:35:VAL:CG1	8:P:47:TYR:HB2	2.42	0.49
8:Q:393:MET:HG3	8:Q:395:CYS:SG	2.52	0.49
1:S:169:GLU:HA	1:S:172:LYS:HD2	1.95	0.49
1:S:1335:PHE:HD2	1:S:1360:MET:HG2	1.76	0.49
10:U:90:ILE:HD11	10:U:128:GLU:HB2	1.94	0.49
10:U:435:MET:N	10:U:435:MET:HE2	2.27	0.49
11:V:163:GLU:N	11:V:163:GLU:OE2	2.46	0.49
11:V:665:VAL:HG13	11:V:695:ILE:HG23	1.92	0.49
1:A:393:VAL:HA	1:A:396:LEU:HD12	1.94	0.49
1:A:751:ARG:HA	1:A:754:CYS:SG	2.52	0.49
6:H:158:ASP:OD1	6:H:159:LEU:N	2.45	0.49
7:M:41:VAL:HB	7:M:52:ARG:HB2	1.94	0.49
2:O:738:LEU:HD13	2:O:742:CYS:SG	2.53	0.49
10:U:206:ASN:O	10:U:209:GLU:HG2	2.12	0.49
10:U:306:SER:N	10:U:309:SER:HB3	2.27	0.49
10:U:1041:SER:CB	10:U:1137:GLN:HE22	2.25	0.49
11:V:383:VAL:HG21	11:V:424:HIS:HD2	1.77	0.49
11:V:477:LEU:O	11:V:481:ILE:HG13	2.11	0.49
1:A:1056:LEU:HD13	1:A:1115:GLU:HG3	1.95	0.49
2:B:239:TYR:HB3	2:B:259:LEU:HD21	1.95	0.49
2:B:287:VAL:HG12	2:B:301:VAL:HG22	1.94	0.49
2:B:524:GLN:O	2:B:580:ALA:HA	2.12	0.49
3:C:434:ASP:OD2	4:E:177:ARG:NH1	2.45	0.49
5:F:283:GLN:HG2	5:F:347:TRP:HZ2	1.78	0.49
6:G:334:LEU:H	6:G:334:LEU:HD23	1.77	0.49
6:H:156:LEU:HB3	6:H:177:LEU:HD11	1.95	0.49
8:P:25:LYS:N	8:P:26:PRO:CD	2.75	0.49
8:P:606:LEU:O	8:P:609:VAL:HG22	2.13	0.49
8:P:850:ARG:NH1	8:P:856:GLU:HB2	2.26	0.49
8:Q:361:SER:OG	8:Q:366:LEU:HG	2.13	0.49
10:U:504:GLN:HG2	10:U:505:PRO:HD3	1.95	0.49
11:V:72:GLN:HE21	11:V:138:LEU:HD21	1.76	0.49
1:A:1099:GLN:CD	1:A:1099:GLN:H	2.15	0.49
2:B:259:LEU:HD11	2:B:284:PRO:HB2	1.95	0.49
3:C:245:ARG:NH2	4:E:92:ARG:HH21	2.10	0.49
4:E:352:SER:O	4:E:353:PRO:O	2.31	0.49
6:H:115:GLU:N	6:H:121:LEU:HD21	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:249:PRO:HD3	7:L:274:TRP:CZ2	2.48	0.49
8:Q:178:TYR:CE2	8:Q:246:PRO:HD2	2.48	0.49
10:U:540:PHE:HA	10:U:543:LEU:HD12	1.93	0.49
11:V:84:ARG:HA	11:V:89:TYR:CE1	2.47	0.49
11:V:210:ASP:O	11:V:213:THR:HG22	2.13	0.49
11:V:412:ILE:HG23	11:V:416:LEU:HD23	1.95	0.49
1:A:136:LEU:HD11	1:A:231:ALA:HB2	1.95	0.49
1:A:929:TYR:HB2	1:A:972:GLY:HA2	1.93	0.49
7:M:275:ASP:O	7:M:283:ASN:ND2	2.44	0.49
1:S:57:LEU:HA	1:S:60:LEU:HB3	1.94	0.49
1:S:166:PHE:O	1:S:170:LEU:HG	2.13	0.49
1:S:341:GLN:HG3	1:S:484:GLU:HB3	1.95	0.49
1:S:567:THR:HG22	1:S:1065:VAL:HG13	1.95	0.49
1:S:1090:LEU:HD13	1:S:1134:PHE:CD1	2.47	0.49
10:U:665:ASP:OD1	10:U:665:ASP:N	2.44	0.49
10:U:1022:ALA:O	10:U:1026:LYS:HG2	2.13	0.49
11:V:134:SER:OG	11:V:137:LYS:HG3	2.12	0.49
11:V:146:GLN:HE22	11:V:186:VAL:HA	1.78	0.49
11:V:920:ASN:OD1	11:V:921:SER:N	2.45	0.49
1:A:287:GLU:O	1:A:289:SER:N	2.46	0.49
1:A:822:LEU:HD11	1:A:833:CYS:HB2	1.94	0.49
6:G:198:GLN:OE1	6:G:203:LEU:HG	2.12	0.49
8:P:74:ARG:HD3	8:P:91:ASP:OD1	2.13	0.49
8:P:220:LEU:HD13	8:P:224:LEU:HD22	1.93	0.49
8:Q:28:VAL:HG22	8:Q:37:LEU:HD13	1.94	0.49
8:Q:364:SER:OG	8:Q:365:ASP:N	2.45	0.49
10:U:418:ALA:O	10:U:421:LEU:HB3	2.12	0.49
6:G:67:LEU:HD21	6:G:103:VAL:HG22	1.95	0.49
6:G:257:ARG:HG3	6:G:289:LEU:HD13	1.95	0.49
6:H:265:ALA:O	6:H:269:LEU:HG	2.13	0.49
2:O:72:SER:OG	2:O:101:LYS:HE3	2.13	0.49
2:O:675:TRP:O	2:O:679:HIS:HB2	2.13	0.49
8:Q:538:ASP:OD1	8:Q:539:GLN:N	2.45	0.49
1:S:186:HIS:CD2	1:S:193:LEU:H	2.26	0.49
1:S:583:PHE:HZ	1:S:613:ILE:HG23	1.78	0.49
1:S:1393:VAL:O	1:S:1397:THR:HG23	2.13	0.49
10:U:600:ASP:N	10:U:600:ASP:OD1	2.45	0.49
10:U:664:LEU:HD13	10:U:667:LEU:HD22	1.95	0.49
11:V:369:GLU:OE1	11:V:398:TYR:OH	2.28	0.49
1:A:677:VAL:HG11	1:A:748:LEU:HB3	1.95	0.49
2:B:39:LYS:HG3	2:B:40:THR:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:514:MET:HA	4:E:517:GLU:HG2	1.94	0.49
6:H:31:GLN:O	6:H:39:ARG:NH1	2.45	0.49
7:M:21:SER:O	7:M:23:THR:N	2.45	0.49
7:M:121:LEU:HG	7:M:125:LYS:HG3	1.95	0.49
8:Q:219:THR:HG21	8:Q:306:ASP:HB3	1.94	0.49
1:S:321:SER:O	1:S:325:THR:HG23	2.12	0.49
1:S:1188:HIS:ND1	1:S:1189:CYS:SG	2.81	0.49
10:U:747:MET:HG2	10:U:778:TYR:CD1	2.48	0.49
10:U:1033:PHE:O	10:U:1037:VAL:HG23	2.13	0.49
1:A:346:TRP:CZ2	1:A:387:GLN:HG2	2.47	0.48
1:A:1168:THR:O	1:A:1171:LEU:HB2	2.12	0.48
1:A:1315:LEU:HB3	1:A:1319:LEU:HD22	1.95	0.48
3:C:60:VAL:HG23	3:C:64:PHE:CE1	2.48	0.48
5:F:83:PHE:HA	5:F:86:LEU:HD13	1.94	0.48
7:M:16:LEU:HD23	7:M:26:GLU:O	2.12	0.48
8:Q:791:SER:HB3	8:Q:797:ILE:HD11	1.94	0.48
10:U:284:GLU:OE1	10:U:284:GLU:N	2.45	0.48
10:U:817:LEU:HD21	10:U:839:MET:HG2	1.95	0.48
10:U:1079:THR:O	10:U:1083:THR:OG1	2.22	0.48
11:V:113:CYS:SG	11:V:135:LEU:HD22	2.53	0.48
11:V:278:LEU:N	11:V:279:PRO:HD2	2.28	0.48
11:V:1343:GLY:O	11:V:1347:ILE:HG13	2.13	0.48
3:C:58:ASN:ND2	3:C:99:ASN:HB2	2.28	0.48
3:C:241:CYS:SG	4:E:37:PRO:HD3	2.49	0.48
1:S:286:GLN:N	1:S:287:GLU:OE1	2.44	0.48
11:V:347:PHE:HA	11:V:350:ILE:HD12	1.95	0.48
11:V:643:LYS:O	11:V:643:LYS:HG2	2.12	0.48
11:V:786:ILE:HG21	11:V:826:LEU:HB2	1.94	0.48
5:F:252:CYS:HB3	5:F:274:TYR:HE1	1.78	0.48
6:G:150:TRP:CE2	6:G:155:ARG:HD2	2.47	0.48
8:P:733:LEU:HD21	8:P:754:ILE:HD13	1.95	0.48
8:Q:366:LEU:HD11	8:Q:401:ILE:HD12	1.96	0.48
1:S:764:ARG:HH12	9:W:95:TRP:HZ3	1.61	0.48
1:A:822:LEU:HD22	1:A:867:LYS:HD3	1.95	0.48
1:A:946:LEU:HD22	1:A:950:GLU:HB3	1.95	0.48
1:A:1257:LEU:HA	1:A:1260:LEU:HG	1.95	0.48
2:B:329:LEU:HD12	2:B:342:LEU:HD23	1.95	0.48
2:O:342:LEU:HD11	2:O:357:PHE:HB2	1.95	0.48
2:O:854:GLN:HB3	8:Q:798:CYS:HB2	1.95	0.48
10:U:117:ARG:HE	10:U:167:GLY:HA3	1.78	0.48
11:V:59:LEU:HD13	11:V:66:ASN:ND2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:660:PHE:CZ	2:B:731:LEU:HD11	2.49	0.48
10:U:4:LYS:HE2	10:U:20:PHE:HZ	1.78	0.48
10:U:237:PHE:CD1	10:U:240:LEU:HD12	2.48	0.48
10:U:654:GLN:OE1	10:U:654:GLN:N	2.46	0.48
10:U:724:ASP:OD2	10:U:725:LYS:NZ	2.40	0.48
10:U:1043:VAL:HA	10:U:1046:LEU:HD12	1.95	0.48
1:A:113:SER:HB2	1:A:155:LEU:HD13	1.93	0.48
1:A:740:GLU:OE1	1:A:849:SER:HB2	2.13	0.48
2:B:25:PHE:HA	2:B:44:HIS:O	2.13	0.48
3:C:186:VAL:O	3:C:186:VAL:CG1	2.61	0.48
6:H:548:ARG:NH2	6:H:606:ASP:OD2	2.46	0.48
7:L:268:SER:O	7:L:271:ILE:HG12	2.12	0.48
7:M:42:LEU:HD21	7:M:80:LEU:HD12	1.94	0.48
2:O:761:PHE:O	2:O:765:LYS:HG2	2.14	0.48
8:P:325:LYS:HG2	8:P:326:ALA:H	1.78	0.48
8:Q:531:ASN:OD1	8:Q:574:PRO:HA	2.13	0.48
1:S:1261:PHE:O	1:S:1265:LEU:HG	2.13	0.48
10:U:341:LEU:HD13	10:U:359:TYR:CE2	2.48	0.48
10:U:723:LEU:O	10:U:725:LYS:HG2	2.13	0.48
11:V:107:GLU:OE1	11:V:111:ARG:NE	2.44	0.48
11:V:429:LYS:HG3	11:V:430:ASP:H	1.78	0.48
11:V:656:ILE:HG23	11:V:733:TYR:CE1	2.48	0.48
4:E:358:SER:O	4:E:361:THR:OG1	2.27	0.48
7:L:64:SER:HA	7:L:67:HIS:NE2	2.28	0.48
8:P:504:ARG:N	8:P:505:PRO:CD	2.77	0.48
1:S:1302:TRP:O	1:S:1305:LEU:HG	2.12	0.48
10:U:776:MET:O	10:U:780:LYS:HG3	2.14	0.48
11:V:777:LYS:O	11:V:781:PHE:CD1	2.66	0.48
1:A:1222:PRO:HG2	1:A:1225:LEU:HD13	1.96	0.48
2:B:673:LYS:NZ	2:B:709:GLN:OE1	2.47	0.48
3:C:457:SER:HB3	3:C:494:PHE:CE1	2.48	0.48
4:E:64:LEU:HD11	4:E:109:LEU:HD22	1.94	0.48
5:F:345:SER:HB2	5:F:348:THR:HG23	1.96	0.48
6:G:266:LEU:HD21	1:S:51:LEU:O	2.12	0.48
2:O:10:ASN:HD21	2:O:74:LEU:H	1.62	0.48
2:O:323:GLU:O	2:O:324:LYS:HG2	2.13	0.48
8:P:253:VAL:HB	8:P:272:VAL:HG22	1.94	0.48
8:Q:337:GLU:OE1	8:Q:383:PRO:HG2	2.13	0.48
1:S:1343:HIS:CE1	1:S:1348:ILE:HB	2.48	0.48
9:W:79:THR:HG22	9:W:80:VAL:H	1.79	0.48
10:U:184:VAL:HG13	10:U:186:LEU:HG	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:450:THR:HG21	11:V:356:TYR:HA	1.95	0.48
1:A:221:MET:HG3	1:A:222:GLU:OE1	2.14	0.48
1:A:1343:HIS:CE1	1:A:1348:ILE:HB	2.49	0.48
4:E:492:LEU:O	4:E:495:THR:OG1	2.28	0.48
6:G:54:LEU:O	6:G:58:GLN:HG3	2.14	0.48
7:L:37:HIS:CD2	7:L:38:LEU:H	2.32	0.48
8:P:145:GLN:HG3	8:P:150:TRP:NE1	2.28	0.48
9:W:76:GLU:HG3	9:W:84:THR:HB	1.96	0.48
10:U:417:HIS:ND1	10:U:420:LYS:HD3	2.29	0.48
10:U:430:PHE:O	10:U:437:ARG:NH2	2.43	0.48
1:A:235:LEU:HD12	1:A:236:SER:N	2.29	0.48
1:A:712:GLU:HG2	1:A:713:PRO:HD2	1.96	0.48
1:A:828:ASP:OD1	1:A:828:ASP:N	2.47	0.48
1:A:1193:LEU:HD23	1:A:1198:GLN:HG3	1.95	0.48
1:A:1367:LEU:HD11	1:A:1372:ASP:HB3	1.95	0.48
2:B:582:THR:HG22	2:B:583:SER:O	2.14	0.48
2:B:747:LEU:HD22	2:B:750:GLY:O	2.14	0.48
6:H:354:CYS:SG	6:H:359:ARG:HB2	2.53	0.48
2:O:312:TRP:CD1	2:O:319:ALA:HB2	2.49	0.48
2:O:328:VAL:HG23	2:O:343:LEU:HD23	1.96	0.48
2:O:679:HIS:O	2:O:681:LYS:NZ	2.46	0.48
8:P:36:PHE:CD2	8:P:46:VAL:HG22	2.48	0.48
8:P:312:LEU:O	8:P:323:ALA:HA	2.14	0.48
8:P:655:PHE:CE2	8:P:754:ILE:HD12	2.49	0.48
8:Q:730:CYS:O	8:Q:734:GLN:HG2	2.14	0.48
1:S:328:LEU:HD11	1:S:384:VAL:HG13	1.96	0.48
1:S:1296:GLU:O	1:S:1299:LYS:NZ	2.43	0.48
1:A:650:LEU:HD21	1:A:714:ARG:NH2	2.24	0.47
1:A:739:PRO:HA	1:A:742:GLN:HB2	1.96	0.47
2:B:240:VAL:HG12	2:B:241:HIS:N	2.28	0.47
2:B:315:SER:O	2:B:317:GLN:N	2.47	0.47
2:B:323:GLU:C	2:B:324:LYS:HD3	2.34	0.47
4:E:465:THR:OG1	4:E:468:LYS:HE2	2.14	0.47
4:E:493:MET:O	4:E:497:MET:HG3	2.14	0.47
6:H:141:ARG:NH1	6:H:196:THR:HG21	2.29	0.47
7:L:54:LEU:HG	7:L:55:CYS:N	2.27	0.47
7:M:272:HIS:CE1	7:M:273:LEU:HG	2.49	0.47
2:O:390:VAL:C	2:O:393:PRO:HD2	2.35	0.47
8:P:28:VAL:HG23	8:P:400:ASN:ND2	2.29	0.47
8:P:870:TYR:CZ	8:P:874:ARG:HG3	2.49	0.47
1:S:424:LEU:HD21	1:S:472:PHE:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:324:ASP:N	10:U:324:ASP:OD1	2.46	0.47
10:U:331:LYS:O	10:U:335:VAL:HG23	2.13	0.47
10:U:835:SER:HB2	10:U:838:PHE:HB3	1.91	0.47
10:U:858:HIS:HB2	10:U:864:GLY:O	2.13	0.47
10:U:1010:THR:HB	10:U:1032:LEU:HD23	1.96	0.47
11:V:382:LEU:HD13	11:V:417:LEU:HD12	1.96	0.47
1:A:264:GLN:HA	1:A:267:VAL:HG12	1.95	0.47
1:A:1335:PHE:HD2	1:A:1360:MET:HG2	1.79	0.47
2:B:846:GLN:HE22	8:P:877:SER:CB	2.22	0.47
3:C:87:GLN:CD	3:C:87:GLN:H	2.17	0.47
3:C:140:TYR:CD2	5:F:169:LEU:HD22	2.50	0.47
3:C:429:TYR:HE1	4:E:176:ARG:HH21	1.62	0.47
6:G:57:LEU:HD22	6:G:66:VAL:HG23	1.96	0.47
6:H:450:LEU:O	6:H:453:SER:OG	2.25	0.47
8:Q:850:ARG:O	8:Q:853:THR:HG22	2.14	0.47
1:S:767:GLN:HE22	1:S:1003:ASN:ND2	2.13	0.47
1:S:815:PRO:HA	1:S:818:PHE:HD2	1.80	0.47
1:S:1102:THR:OG1	1:S:1158:LYS:HE3	2.14	0.47
9:W:78:PHE:HA	9:W:82:PRO:HB3	1.95	0.47
10:U:1138:LEU:HD13	10:U:1176:LEU:HD11	1.96	0.47
11:V:686:LEU:HB3	11:V:688:GLU:OE1	2.14	0.47
11:V:845:VAL:O	11:V:848:LEU:HG	2.15	0.47
1:A:171:TRP:CD2	1:A:200:HIS:HD2	2.32	0.47
1:A:405:GLN:OE1	1:A:405:GLN:N	2.46	0.47
1:A:1406:LEU:O	1:A:1409:ARG:N	2.46	0.47
2:B:526:ARG:NH1	2:B:653:ALA:O	2.48	0.47
6:G:177:LEU:HD12	6:G:211:PHE:CZ	2.49	0.47
6:G:565:ASP:OD1	6:G:565:ASP:N	2.47	0.47
7:L:309:ILE:HD11	7:L:360:PRO:HG2	1.97	0.47
7:M:101:LEU:HD21	8:Q:339:ARG:HG3	1.95	0.47
2:O:662:ILE:HG12	2:O:744:LEU:HD13	1.95	0.47
2:O:724:GLN:HG2	2:O:727:MET:HE3	1.97	0.47
10:U:706:LEU:O	10:U:710:THR:HG23	2.13	0.47
11:V:220:GLY:N	11:V:223:GLN:HE22	2.13	0.47
11:V:500:VAL:HG12	11:V:507:MET:HG2	1.96	0.47
11:V:569:LYS:HD3	11:V:851:THR:HG22	1.96	0.47
1:A:1165:LEU:HD11	1:A:1322:VAL:HA	1.96	0.47
7:M:101:LEU:HD21	8:Q:339:ARG:NE	2.30	0.47
7:M:307:CYS:HB2	7:M:334:HIS:CE1	2.50	0.47
2:O:40:THR:HG21	2:O:67:ILE:HB	1.96	0.47
8:P:325:LYS:HB2	8:P:384:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:P:399:LEU:O	8:P:400:ASN:HB3	2.14	0.47
8:Q:292:PRO:HG3	8:Q:355:GLY:HA2	1.97	0.47
1:S:346:TRP:CE2	1:S:387:GLN:HG2	2.49	0.47
1:S:474:PHE:O	1:S:478:SER:N	2.41	0.47
10:U:106:VAL:O	10:U:110:ASN:ND2	2.47	0.47
10:U:447:ARG:HD3	10:U:459:PHE:CZ	2.49	0.47
10:U:547:PHE:HB2	10:U:550:LEU:HD11	1.97	0.47
10:U:1269:LYS:HG3	10:U:1270:LYS:HG3	1.95	0.47
11:V:1283:LYS:H	11:V:1283:LYS:HD2	1.78	0.47
1:A:1265:LEU:HD23	1:A:1288:CYS:SG	2.55	0.47
2:B:15:LEU:HD22	2:B:24:VAL:HG22	1.95	0.47
2:B:79:CYS:CB	2:B:94:ILE:HD13	2.45	0.47
4:E:118:LEU:HD21	4:E:140:LEU:HD23	1.96	0.47
4:E:523:LEU:HD22	11:V:158:PRO:CG	2.45	0.47
2:O:73:HIS:CB	2:O:99:ASN:HB3	2.45	0.47
8:P:60:PHE:HZ	8:P:88:LEU:HD11	1.79	0.47
1:S:587:LEU:HD12	1:S:617:LEU:HB3	1.96	0.47
1:S:1210:PHE:HD2	1:S:1230:LEU:HD11	1.79	0.47
11:V:417:LEU:HD13	11:V:453:PHE:CZ	2.50	0.47
1:A:163:ARG:HB2	8:P:849:ASP:OD2	2.14	0.47
1:A:1027:ASP:HA	1:A:1030:LEU:HD21	1.96	0.47
3:C:258:PHE:CD1	3:C:261:LEU:HD21	2.49	0.47
6:G:510:GLN:NE2	6:G:543:MET:HG3	2.29	0.47
6:H:127:ARG:HA	6:H:130:CYS:SG	2.54	0.47
6:H:164:GLU:HG3	6:H:171:SER:O	2.15	0.47
2:O:215:TYR:OH	2:O:219:SER:HA	2.14	0.47
1:S:675:ALA:O	1:S:679:VAL:HG23	2.14	0.47
1:S:911:TRP:O	1:S:917:ARG:HD3	2.15	0.47
1:S:947:SER:N	1:S:950:GLU:OE2	2.41	0.47
11:V:173:PRO:O	11:V:176:ILE:HG22	2.15	0.47
11:V:791:ASN:OD1	11:V:925:PHE:HA	2.15	0.47
1:A:31:LYS:HD2	6:H:380:PRO:HG3	1.97	0.47
1:A:393:VAL:O	1:A:397:VAL:HG13	2.15	0.47
2:B:11:GLU:HG3	2:B:12:GLN:HG2	1.97	0.47
2:B:272:THR:O	2:B:274:LYS:N	2.48	0.47
3:C:58:ASN:OD1	3:C:107:GLN:HG2	2.14	0.47
4:E:379:ALA:HB2	4:E:419:LEU:HD21	1.96	0.47
6:G:31:GLN:HE21	6:G:321:PHE:N	2.13	0.47
6:G:176:ASP:O	6:G:180:LEU:HD23	2.15	0.47
6:G:344:SER:OG	6:G:383:SER:HB3	2.15	0.47
7:L:307:CYS:HB2	7:L:334:HIS:ND1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:28:PHE:CE1	2:O:418:ILE:HG13	2.49	0.47
7:M:107:PRO:CG	7:M:108:PRO:CD	2.92	0.47
2:O:603:GLU:HG3	2:O:611:LYS:CE	2.45	0.47
8:P:60:PHE:CZ	8:P:88:LEU:HD11	2.49	0.47
8:P:66:HIS:CD2	8:P:67:LEU:N	2.83	0.47
8:P:835:ALA:O	8:P:839:THR:HG22	2.14	0.47
1:S:36:ASN:ND2	1:S:39:ARG:HB2	2.30	0.47
1:S:185:LEU:HD11	1:S:191:VAL:HG23	1.96	0.47
1:S:940:GLN:HA	1:S:1013:GLY:HA2	1.97	0.47
1:S:966:GLU:HA	1:S:974:ASP:OD1	2.14	0.47
1:S:1303:LEU:HA	1:S:1306:PHE:CD2	2.50	0.47
1:S:1336:TYR:CB	1:S:1395:LEU:HD11	2.45	0.47
10:U:424:ASN:O	10:U:428:GLU:HG2	2.14	0.47
10:U:832:LEU:HB3	10:U:838:PHE:CE2	2.50	0.47
10:U:1081:ALA:HB3	10:U:1082:PRO:HD3	1.97	0.47
11:V:60:LYS:NZ	11:V:63:GLU:HB3	2.28	0.47
11:V:562:GLN:O	11:V:565:SER:OG	2.22	0.47
1:A:747:ALA:O	1:A:750:VAL:HG22	2.14	0.47
1:A:1299:LYS:NZ	1:A:1348:ILE:HD11	2.30	0.47
1:A:1415:PHE:O	1:A:1418:VAL:HG22	2.15	0.47
2:B:529:LYS:HG2	2:B:576:GLN:HG3	1.96	0.47
2:B:655:PHE:CZ	2:B:722:ARG:HB3	2.50	0.47
3:C:485:GLN:HG2	3:C:488:ARG:HH11	1.80	0.47
4:E:149:SER:OG	4:E:151:GLU:OE2	2.33	0.47
6:H:267:LEU:O	6:H:270:VAL:HG22	2.15	0.47
7:L:107:PRO:N	7:L:108:PRO:HD2	2.30	0.47
8:P:557:ASP:OD1	8:P:557:ASP:N	2.48	0.47
11:V:175:LEU:O	11:V:178:SER:OG	2.19	0.47
11:V:1038:ALA:HA	11:V:1041:ASN:HD21	1.80	0.47
11:V:1054:GLU:HA	11:V:1057:ILE:HG12	1.96	0.47
11:V:1105:GLN:NE2	11:V:1109:GLU:HG3	2.30	0.47
1:A:963:PHE:HE1	1:A:980:ALA:HB2	1.80	0.47
1:A:1085:LEU:HB3	1:A:1086:PRO:HD2	1.97	0.47
1:A:1313:LEU:HA	1:A:1317:ARG:HG2	1.97	0.47
2:B:146:HIS:CE1	2:B:151:PHE:HE2	2.33	0.47
2:B:680:MET:HE1	2:B:696:ARG:HH11	1.80	0.47
2:B:770:LEU:O	2:B:773:LEU:HB3	2.15	0.47
6:G:16:TRP:CZ3	6:G:60:LEU:HD11	2.50	0.47
6:G:117:GLY:O	6:G:121:LEU:HD23	2.15	0.47
6:G:601:ARG:HD3	6:G:605:ARG:CZ	2.45	0.47
8:P:288:LEU:HB2	8:P:311:CYS:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:P:346:PRO:O	8:P:363:PRO:HD3	2.15	0.47
8:P:712:ALA:H	8:P:782:ILE:CG2	2.28	0.47
8:Q:366:LEU:O	8:Q:393:MET:HG2	2.15	0.47
8:Q:569:VAL:HG11	8:Q:572:LEU:HD12	1.97	0.47
8:Q:570:ASP:C	8:Q:572:LEU:H	2.18	0.47
1:S:190:ILE:HG22	1:S:191:VAL:HG23	1.97	0.47
1:S:337:SER:OG	1:S:428:VAL:HG11	2.15	0.47
1:S:449:ALA:HB2	1:S:492:HIS:CE1	2.49	0.47
1:S:929:TYR:CZ	1:S:933:LEU:HD21	2.50	0.47
1:S:1083:LEU:HD11	1:S:1129:ASP:OD1	2.15	0.47
1:S:1126:LEU:H	1:S:1169:SER:HB3	1.80	0.47
10:U:179:SER:O	10:U:182:LYS:HE3	2.14	0.47
10:U:446:ASN:ND2	11:V:355:ARG:HE	2.12	0.47
1:A:61:LEU:HD12	1:A:77:VAL:CG2	2.44	0.47
1:A:1142:CYS:SG	1:A:1143:LEU:N	2.88	0.47
2:B:821:LYS:O	2:B:825:GLN:HG3	2.15	0.47
4:E:106:ARG:NE	4:E:143:ASP:OD1	2.48	0.47
6:H:12:CYS:SG	2:O:205:TYR:HD2	2.38	0.47
6:H:564:ARG:HG3	6:H:565:ASP:H	1.79	0.47
7:L:321:ASP:O	7:L:323:VAL:HG13	2.15	0.47
8:P:148:ALA:O	8:P:180:PRO:HD2	2.15	0.47
8:P:349:CYS:SG	8:P:401:ILE:HG22	2.55	0.47
8:P:586:PRO:HB2	8:P:590:GLY:HA2	1.97	0.47
8:P:717:ALA:HB3	8:P:815:GLN:HE22	1.79	0.47
8:Q:28:VAL:HG12	8:Q:402:CYS:SG	2.55	0.47
8:Q:324:ILE:HG12	8:Q:338:LEU:HD22	1.96	0.47
8:Q:495:ALA:CB	8:Q:505:PRO:HG3	2.45	0.47
1:S:360:ARG:O	1:S:364:VAL:HG23	2.15	0.47
1:S:414:LEU:HD21	1:S:426:SER:HB2	1.96	0.47
1:S:757:VAL:O	1:S:761:VAL:HG23	2.15	0.47
1:S:929:TYR:O	1:S:933:LEU:HG	2.14	0.47
1:S:1287:VAL:O	1:S:1291:ILE:HG12	2.15	0.47
1:A:137:LEU:HB2	1:A:141:GLN:OE1	2.16	0.46
1:A:469:ALA:O	1:A:473:LEU:HG	2.16	0.46
1:A:875:LEU:HD11	1:A:945:ALA:HB1	1.96	0.46
2:B:150:PHE:CE2	2:B:167:PHE:HB2	2.50	0.46
2:B:228:ILE:HG22	2:B:229:ILE:H	1.80	0.46
3:C:151:LYS:HE2	3:C:155:LEU:HD13	1.96	0.46
4:E:491:LYS:NZ	11:V:202:ILE:O	2.45	0.46
6:G:137:SER:HA	6:G:187:PRO:HG2	1.97	0.46
6:G:398:LEU:HD22	6:G:458:LEU:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:606:ASP:HA	6:G:609:LEU:HB2	1.97	0.46
2:O:592:LYS:HA	2:O:622:LEU:O	2.14	0.46
2:O:734:LEU:O	2:O:737:ILE:HG22	2.14	0.46
1:S:843:TYR:HA	1:S:846:CYS:SG	2.55	0.46
10:U:15:ASP:OD2	10:U:16:LYS:NZ	2.42	0.46
11:V:190:LYS:CD	11:V:190:LYS:H	2.27	0.46
11:V:558:VAL:HG22	11:V:562:GLN:NE2	2.26	0.46
1:A:494:LEU:CD1	1:A:518:LEU:HD12	2.46	0.46
1:A:1030:LEU:HD22	1:S:1140:ASN:ND2	2.31	0.46
1:A:1069:LEU:HD12	1:A:1070:GLN:N	2.30	0.46
2:B:231:PRO:HA	2:B:234:SER:HB3	1.95	0.46
2:O:122:LEU:HD21	2:O:155:SER:HA	1.97	0.46
2:O:482:VAL:HG13	2:O:584:LEU:HD11	1.96	0.46
8:P:431:THR:O	8:P:431:THR:OG1	2.27	0.46
8:P:479:ARG:HG3	8:P:479:ARG:NH2	2.30	0.46
8:P:516:ARG:O	8:P:517:LEU:HD22	2.15	0.46
1:S:218:CYS:HB3	1:S:294:ILE:HA	1.97	0.46
1:S:553:LYS:O	1:S:557:VAL:HG12	2.14	0.46
9:W:77:VAL:HB	9:W:85:PHE:CD2	2.50	0.46
10:U:467:VAL:HG22	10:U:474:LEU:HD11	1.97	0.46
11:V:1025:ASN:OD1	11:V:1026:HIS:N	2.48	0.46
1:A:397:VAL:HG12	1:A:407:LEU:HD22	1.96	0.46
2:B:622:LEU:HD23	2:B:622:LEU:HA	1.61	0.46
3:C:162:ARG:HH12	3:C:166:LEU:HG	1.80	0.46
6:G:534:LEU:HD12	6:G:538:LEU:HD23	1.96	0.46
7:L:109:GLN:HE22	7:L:159:PRO:HG2	1.80	0.46
7:M:57:TRP:CE2	8:Q:277:HIS:HB3	2.51	0.46
8:Q:724:SER:OG	8:Q:725:GLY:N	2.48	0.46
1:S:653:LEU:O	1:S:657:LEU:HG	2.15	0.46
1:S:983:ILE:HA	1:S:986:ASN:HD22	1.80	0.46
10:U:879:ARG:NH1	10:U:933:ALA:HB1	2.30	0.46
11:V:72:GLN:NE2	11:V:138:LEU:HD21	2.30	0.46
11:V:208:GLN:O	11:V:212:ILE:HG22	2.15	0.46
11:V:1197:LEU:HD13	11:V:1270:MET:HG3	1.98	0.46
2:B:17:CYS:O	2:B:17:CYS:SG	2.74	0.46
7:M:146:ARG:HD3	7:M:205:ASP:OD2	2.15	0.46
8:Q:243:CYS:SG	8:Q:251:CYS:HB2	2.56	0.46
8:Q:655:PHE:HD1	8:Q:756:GLY:HA3	1.79	0.46
1:S:185:LEU:HD21	1:S:191:VAL:HB	1.97	0.46
1:S:1075:LEU:HD11	1:S:1115:GLU:HB3	1.97	0.46
1:S:1299:LYS:HZ1	1:S:1348:ILE:HD11	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:871:PHE:HE2	10:U:929:GLN:HE21	1.64	0.46
10:U:1054:HIS:CD2	10:U:1151:THR:HG22	2.51	0.46
10:U:1056:HIS:CE1	10:U:1069:THR:HG22	2.50	0.46
10:U:1086:LEU:O	10:U:1089:LEU:HG	2.15	0.46
11:V:485:ASN:OD1	11:V:485:ASN:N	2.48	0.46
11:V:652:VAL:O	11:V:656:ILE:HG12	2.16	0.46
11:V:1021:THR:OG1	11:V:1022:PRO:HD3	2.14	0.46
2:B:711:THR:O	2:B:711:THR:OG1	2.33	0.46
2:B:723:ASN:OD1	2:B:723:ASN:N	2.46	0.46
4:E:400:SER:HA	4:E:440:GLN:HE22	1.79	0.46
5:F:42:ARG:NH2	5:F:127:GLU:O	2.49	0.46
7:M:98:ARG:HG2	7:M:101:LEU:HD12	1.98	0.46
8:P:150:TRP:CD2	8:P:178:TYR:HE2	2.33	0.46
8:P:223:ALA:HB1	8:P:328:TRP:HZ3	1.80	0.46
8:P:778:PRO:HD3	8:P:824:ASP:O	2.15	0.46
1:S:174:GLN:HA	1:S:177:LEU:HD12	1.97	0.46
1:S:1292:LEU:O	1:S:1296:GLU:HG2	2.16	0.46
10:U:87:SER:HB2	11:V:560:ARG:NH2	2.31	0.46
1:A:897:HIS:ND1	1:A:898:LEU:HG	2.30	0.46
3:C:553:GLU:O	3:C:556:THR:OG1	2.26	0.46
6:G:261:ASN:HB3	1:S:63:GLU:OE1	2.16	0.46
6:H:13:LEU:HD23	6:H:14:ASP:H	1.81	0.46
6:H:21:ASP:OD1	6:H:195:LEU:HD13	2.16	0.46
6:H:558:LEU:HD11	6:H:567:ALA:HB2	1.98	0.46
8:Q:92:HIS:CE1	8:Q:116:ILE:HD13	2.51	0.46
1:S:584:LEU:O	1:S:588:LEU:HG	2.16	0.46
1:S:600:ARG:O	1:S:604:ILE:HG12	2.16	0.46
10:U:356:HIS:ND1	10:U:356:HIS:O	2.48	0.46
10:U:642:LEU:O	10:U:644:PRO:HD3	2.14	0.46
10:U:1036:HIS:HE1	10:U:1042:PRO:HA	1.80	0.46
11:V:342:CYS:SG	11:V:343:ILE:N	2.88	0.46
11:V:358:LYS:HD3	11:V:358:LYS:HA	1.61	0.46
11:V:794:ARG:HG2	11:V:928:LEU:HD11	1.97	0.46
7:M:118:ILE:HD11	7:M:126:LEU:HB2	1.97	0.46
2:O:249:LYS:HB3	2:O:250:ASN:H	1.62	0.46
1:S:517:ARG:O	1:S:521:LEU:HG	2.15	0.46
1:S:937:LEU:HA	1:S:1014:ASN:ND2	2.31	0.46
11:V:384:MET:HA	11:V:384:MET:HE2	1.98	0.46
1:A:415:MET:CE	1:A:427:MET:HA	2.41	0.46
1:A:486:PRO:HG2	1:A:489:LEU:HB2	1.98	0.46
4:E:291:LEU:HD23	4:E:312:GLU:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:538:LEU:HD12	6:H:539:LEU:HG	1.96	0.46
7:L:169:PHE:CZ	7:L:173:PHE:HB2	2.51	0.46
7:L:322:GLN:O	7:L:333:PHE:N	2.48	0.46
2:O:66:THR:O	2:O:68:LYS:NZ	2.48	0.46
2:O:141:LEU:HD21	2:O:217:LEU:HD21	1.97	0.46
8:P:220:LEU:HD13	8:P:224:LEU:CD2	2.46	0.46
8:P:448:THR:O	8:P:450:SER:N	2.48	0.46
8:P:538:ASP:HA	8:P:571:GLN:HA	1.97	0.46
8:P:655:PHE:N	8:P:655:PHE:CD1	2.81	0.46
1:S:149:LEU:HD12	1:S:190:ILE:HG13	1.97	0.46
10:U:102:GLY:HA3	10:U:144:LEU:HD21	1.97	0.46
1:A:196:LEU:HD23	1:A:196:LEU:HA	1.72	0.46
1:A:818:PHE:HA	1:A:821:LEU:HD12	1.97	0.46
6:H:79:ILE:CG1	6:H:145:LEU:HD21	2.46	0.46
2:O:780:HIS:ND1	2:O:830:VAL:HG13	2.31	0.46
8:P:28:VAL:N	8:P:400:ASN:HD21	2.14	0.46
1:S:460:ARG:HA	1:S:463:HIS:NE2	2.31	0.46
1:S:758:LEU:O	1:S:762:LEU:HG	2.16	0.46
10:U:298:GLN:NE2	10:U:1104:THR:O	2.49	0.46
10:U:1266:HIS:HA	10:U:1269:LYS:HE3	1.98	0.46
11:V:83:LEU:O	11:V:92:ILE:HD11	2.16	0.46
11:V:282:ILE:O	11:V:286:LEU:HG	2.15	0.46
11:V:766:GLU:HG2	11:V:767:PRO:HD2	1.98	0.46
1:A:474:PHE:HA	1:A:477:LEU:HB2	1.98	0.46
2:B:605:GLU:HG3	2:B:606:SER:N	2.31	0.46
7:M:3:VAL:CG2	7:M:5:GLU:HG2	2.46	0.46
2:O:179:LEU:HD22	2:O:223:LEU:HD11	1.98	0.46
8:Q:54:LEU:HD11	8:Q:114:PRO:HB2	1.97	0.46
1:S:206:VAL:O	1:S:210:LEU:HG	2.16	0.46
1:S:552:GLU:O	1:S:556:MET:HG2	2.16	0.46
10:U:187:THR:HG22	10:U:190:GLU:HG3	1.97	0.46
10:U:295:VAL:O	10:U:297:GLN:N	2.46	0.46
10:U:430:PHE:O	10:U:437:ARG:NE	2.44	0.46
11:V:220:GLY:H	11:V:223:GLN:HE22	1.63	0.46
1:A:1335:PHE:CD2	1:A:1360:MET:HG2	2.51	0.45
4:E:292:GLN:O	4:E:296:LYS:HG2	2.16	0.45
4:E:489:TYR:CE2	4:E:493:MET:HG3	2.51	0.45
5:F:142:ALA:O	5:F:146:LEU:HD23	2.16	0.45
7:L:295:ARG:HB3	7:L:298:LEU:HG	1.98	0.45
7:L:320:PRO:HB2	7:L:332:PRO:HB2	1.98	0.45
2:O:10:ASN:ND2	2:O:74:LEU:HB2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:210:THR:CG2	2:O:228:ILE:HB	2.46	0.45
2:O:345:PHE:HE2	2:O:358:LYS:HB2	1.80	0.45
8:P:322:LEU:HA	8:P:339:ARG:O	2.16	0.45
8:Q:589:ASN:HD22	8:Q:675:PRO:HD3	1.80	0.45
1:S:862:PRO:O	1:S:866:LYS:HG2	2.15	0.45
1:S:877:SER:HA	1:S:880:ARG:HE	1.80	0.45
11:V:686:LEU:HD12	11:V:757:ASP:HA	1.98	0.45
11:V:1088:TYR:CE1	11:V:1107:LEU:HD13	2.51	0.45
11:V:1313:LEU:O	11:V:1317:PHE:HB2	2.16	0.45
1:A:1272:HIS:CE1	1:A:1333:PHE:HE2	2.34	0.45
2:B:857:SER:OG	8:P:867:LEU:HD13	2.16	0.45
4:E:338:ASP:N	4:E:338:ASP:OD1	2.46	0.45
4:E:429:LEU:HB3	4:E:460:ARG:NH1	2.31	0.45
4:E:506:GLU:OE2	4:E:509:ARG:NH2	2.40	0.45
6:G:483:LEU:HD21	6:G:512:LEU:HD23	1.99	0.45
2:O:7:MET:N	2:O:13:GLU:O	2.48	0.45
8:P:767:ILE:HG12	8:P:788:GLN:HB3	1.97	0.45
8:Q:125:LEU:HD23	8:Q:166:PRO:HB3	1.99	0.45
10:U:66:ARG:HG3	10:U:104:LEU:HD22	1.98	0.45
10:U:295:VAL:CG2	10:U:301:SER:HA	2.46	0.45
11:V:71:ASP:OD1	11:V:72:GLN:N	2.48	0.45
11:V:728:LEU:HD23	11:V:840:LEU:HD21	1.97	0.45
11:V:1246:VAL:O	11:V:1249:ILE:HG22	2.17	0.45
11:V:1375:LEU:HD12	11:V:1376:THR:N	2.32	0.45
1:A:299:PHE:CD1	1:A:358:LEU:HD13	2.51	0.45
1:A:477:LEU:HD23	1:A:480:LEU:HD12	1.98	0.45
1:A:746:ALA:O	1:A:750:VAL:HG13	2.16	0.45
1:A:1234:ILE:O	1:A:1237:VAL:HG12	2.15	0.45
1:A:1326:GLN:O	1:A:1330:LEU:HD13	2.15	0.45
2:B:78:CYS:SG	2:B:136:VAL:HG23	2.55	0.45
2:B:764:GLU:O	2:B:768:VAL:HG23	2.15	0.45
3:C:227:ILE:HD11	3:C:239:VAL:HG12	1.98	0.45
5:F:341:VAL:HG13	5:F:342:PRO:HD2	1.97	0.45
6:G:430:LYS:HE2	8:P:332:GLY:HA2	1.98	0.45
7:M:254:LEU:HD22	7:M:321:ASP:HB2	1.98	0.45
2:O:57:PHE:CG	2:O:354:LEU:HD21	2.51	0.45
2:O:767:LEU:HB3	8:Q:841:LEU:HB2	1.97	0.45
8:P:572:LEU:HA	8:P:578:ARG:NH2	2.32	0.45
8:P:713:GLU:HB3	8:P:782:ILE:HD11	1.97	0.45
8:Q:572:LEU:O	8:Q:572:LEU:HD23	2.17	0.45
8:Q:848:ARG:O	8:Q:851:LEU:HG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:214:VAL:O	10:U:218:LEU:HD23	2.15	0.45
10:U:395:PRO:HD2	10:U:458:HIS:CE1	2.51	0.45
10:U:653:THR:HG23	10:U:658:ILE:HB	1.97	0.45
10:U:751:GLU:O	10:U:754:ILE:HB	2.16	0.45
11:V:646:PRO:O	11:V:649:LEU:HB2	2.17	0.45
1:A:171:TRP:CE3	1:A:200:HIS:HD2	2.34	0.45
1:A:424:LEU:O	1:A:428:VAL:HG23	2.16	0.45
1:A:856:LEU:HA	1:A:859:CYS:SG	2.56	0.45
2:B:31:ASN:O	2:B:38:THR:N	2.50	0.45
2:B:252:LEU:HD13	2:B:254:ILE:HG23	1.96	0.45
5:F:246:GLU:O	5:F:249:ALA:HB3	2.16	0.45
6:G:228:ALA:O	6:G:232:LEU:HD23	2.16	0.45
6:G:266:LEU:HD23	1:S:55:GLN:HB2	1.97	0.45
2:O:181:MET:CB	2:O:217:LEU:HD23	2.46	0.45
2:O:217:LEU:HD12	2:O:217:LEU:HA	1.70	0.45
8:P:851:LEU:HD21	8:P:862:THR:HG21	1.99	0.45
10:U:706:LEU:HA	10:U:709:ILE:HD12	1.97	0.45
1:A:824:CYS:SG	1:A:825:ARG:N	2.89	0.45
1:A:1408:PRO:O	1:A:1439:ARG:NH1	2.50	0.45
1:A:1433:SER:O	1:A:1436:LEU:HG	2.16	0.45
2:B:524:GLN:OE1	2:B:581:VAL:HG13	2.16	0.45
6:G:177:LEU:HB2	6:G:211:PHE:CE2	2.52	0.45
8:P:287:ALA:HA	8:P:311:CYS:O	2.16	0.45
8:P:305:GLU:O	8:P:307:VAL:HG23	2.17	0.45
1:S:402:GLU:OE2	1:S:405:GLN:NE2	2.38	0.45
10:U:533:ARG:NE	10:U:597:GLN:HE22	2.14	0.45
10:U:1010:THR:HG21	10:U:1031:LEU:HD21	1.99	0.45
11:V:634:GLU:OE2	11:V:634:GLU:HA	2.16	0.45
11:V:933:PHE:HB2	11:V:1019:LEU:HD13	1.98	0.45
1:A:680:ILE:HG12	1:A:683:ARG:HH22	1.80	0.45
2:B:73:HIS:HB3	2:B:99:ASN:HB3	1.97	0.45
2:B:298:PHE:HE1	2:B:312:TRP:CD1	2.35	0.45
2:B:707:TRP:CH2	2:B:715:GLY:HA3	2.51	0.45
3:C:227:ILE:HD13	3:C:239:VAL:HG12	1.97	0.45
6:G:424:THR:O	6:G:428:LEU:HG	2.16	0.45
7:M:29:ILE:HD11	7:M:88:LYS:HZ2	1.80	0.45
7:M:233:ASN:ND2	7:M:330:GLY:O	2.50	0.45
8:P:66:HIS:HD2	8:P:67:LEU:N	2.14	0.45
8:Q:538:ASP:HA	8:Q:571:GLN:HA	1.99	0.45
1:S:113:SER:O	1:S:117:VAL:HG23	2.16	0.45
1:S:813:PRO:HB2	1:S:815:PRO:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:291:LYS:HA	10:U:294:LYS:HE2	1.98	0.45
10:U:456:ILE:O	10:U:460:LEU:HD12	2.17	0.45
2:B:107:TYR:OH	2:B:130:MET:HG3	2.16	0.45
2:B:242:ILE:HG22	2:B:243:CYS:N	2.32	0.45
2:B:266:ILE:HD12	2:B:268:PHE:CZ	2.52	0.45
2:B:669:LEU:HD12	2:B:669:LEU:HA	1.66	0.45
3:C:49:TYR:CZ	3:C:53:LYS:HD3	2.52	0.45
3:C:122:LEU:O	5:F:140:ARG:CZ	2.65	0.45
3:C:330:SER:O	3:C:330:SER:OG	2.31	0.45
6:G:273:LEU:HD23	6:G:279:TRP:HB2	1.99	0.45
6:H:461:GLN:HG2	6:H:596:TYR:HE1	1.81	0.45
2:O:184:LEU:HD11	2:O:242:ILE:HD11	1.97	0.45
2:O:508:LEU:HD12	2:O:523:CYS:SG	2.56	0.45
8:Q:328:TRP:HB3	8:Q:334:LEU:HD13	1.98	0.45
1:S:795:ARG:HA	1:S:798:LEU:HD12	1.99	0.45
1:S:947:SER:OG	1:S:948:ASP:N	2.49	0.45
10:U:306:SER:H	10:U:309:SER:HB3	1.80	0.45
11:V:637:ASN:C	11:V:641:HIS:ND1	2.63	0.45
1:A:651:GLY:O	1:A:654:THR:OG1	2.35	0.45
1:A:1017:ILE:O	1:A:1021:LEU:HG	2.17	0.45
2:B:657:LYS:HD2	2:B:720:TYR:CE2	2.52	0.45
6:G:342:THR:HG22	6:G:343:GLN:N	2.32	0.45
8:P:763:ASN:O	8:P:791:SER:HB2	2.16	0.45
8:Q:424:SER:OG	8:Q:428:ARG:HB2	2.17	0.45
1:S:151:PHE:O	1:S:155:LEU:HG	2.17	0.45
1:S:358:LEU:O	1:S:362:LEU:HG	2.17	0.45
1:S:616:SER:O	1:S:620:THR:HG23	2.16	0.45
10:U:12:LYS:HA	10:U:12:LYS:HD2	1.81	0.45
10:U:460:LEU:HD12	10:U:460:LEU:H	1.82	0.45
10:U:658:ILE:HG23	10:U:737:ILE:HG21	1.99	0.45
10:U:969:LEU:O	10:U:972:SER:OG	2.25	0.45
11:V:1128:PHE:HB2	11:V:1177:ILE:HG12	1.99	0.45
11:V:1227:THR:OG1	11:V:1228:ARG:N	2.49	0.45
11:V:1291:LEU:O	11:V:1295:LEU:HD13	2.17	0.45
11:V:1299:ARG:NH1	11:V:1359:LEU:HD12	2.28	0.45
6:G:60:LEU:HD12	6:G:66:VAL:HG21	1.99	0.45
7:L:272:HIS:CE1	7:L:273:LEU:HG	2.52	0.45
7:M:239:GLU:O	7:M:249:PRO:HB2	2.16	0.45
7:M:307:CYS:CB	7:M:310:CYS:SG	3.04	0.45
2:O:175:GLU:HA	2:O:180:GLY:O	2.16	0.45
1:S:558:PHE:HD1	1:S:564:ILE:H	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:995:SER:HA	1:S:998:TYR:CE2	2.52	0.45
10:U:36:GLN:HB2	10:U:81:LEU:HD22	1.99	0.45
1:A:265:VAL:O	1:A:269:VAL:HG23	2.17	0.45
1:A:1080:ARG:CZ	1:S:952:GLN:HB2	2.47	0.45
1:A:1416:SER:OG	1:A:1417:HIS:ND1	2.41	0.45
2:B:521:LEU:HD23	2:B:521:LEU:C	2.37	0.45
2:B:522:LYS:HE2	8:P:563:ILE:HG21	1.99	0.45
5:F:23:VAL:HG13	5:F:26:TRP:CD1	2.53	0.45
2:O:356:SER:HA	2:O:369:SER:OG	2.17	0.45
8:Q:150:TRP:HE1	8:Q:180:PRO:HG3	1.82	0.45
1:S:494:LEU:HD11	1:S:518:LEU:HD11	1.99	0.45
1:S:576:ARG:N	1:S:577:PRO:HD2	2.32	0.45
1:S:803:VAL:HA	9:W:4:UNK:HA	1.98	0.45
1:S:932:TRP:CE3	1:S:933:LEU:HD23	2.51	0.45
10:U:413:MET:SD	10:U:417:HIS:CD2	3.09	0.45
11:V:60:LYS:CE	11:V:61:THR:HG22	2.47	0.45
11:V:546:GLU:N	11:V:546:GLU:OE1	2.50	0.45
11:V:555:MET:HA	11:V:558:VAL:HG12	1.98	0.45
11:V:678:PHE:HB3	11:V:763:THR:OG1	2.17	0.45
1:A:191:VAL:HG12	1:A:192:SER:N	2.32	0.44
2:B:520:LEU:HD21	8:P:565:TYR:CD2	2.52	0.44
4:E:469:PHE:O	4:E:473:MET:HG2	2.17	0.44
6:G:152:SER:OG	6:G:328:LEU:HD23	2.17	0.44
6:G:392:CYS:SG	6:G:395:GLU:HG3	2.57	0.44
2:O:290:MET:HE1	2:O:341:VAL:HB	1.98	0.44
8:P:158:PRO:HD2	8:P:165:ARG:O	2.16	0.44
8:Q:39:THR:OG1	8:Q:41:SER:OG	2.23	0.44
8:Q:315:PHE:CZ	8:Q:321:MET:SD	3.11	0.44
8:Q:735:TRP:CH2	8:Q:811:MET:HB2	2.52	0.44
1:S:936:GLU:OE2	1:S:1014:ASN:ND2	2.50	0.44
10:U:882:LEU:HD13	10:U:934:LEU:HD22	1.98	0.44
11:V:364:TRP:HZ2	11:V:380:PHE:HE1	1.65	0.44
11:V:414:GLU:O	11:V:417:LEU:N	2.50	0.44
1:A:182:VAL:HG23	1:A:196:LEU:HD12	1.98	0.44
2:B:259:LEU:N	2:B:259:LEU:HD23	2.32	0.44
4:E:409:ALA:O	4:E:412:THR:OG1	2.35	0.44
5:F:6:GLN:O	5:F:10:ARG:HB2	2.16	0.44
7:L:116:GLU:O	7:L:120:THR:HG23	2.16	0.44
7:M:170:PRO:HG3	7:M:200:PHE:CE2	2.52	0.44
2:O:134:LEU:CD1	2:O:142:ILE:HG23	2.47	0.44
8:P:655:PHE:CZ	8:P:754:ILE:HD12	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:P:708:ILE:O	8:P:786:GLU:HA	2.17	0.44
1:S:290:SER:C	1:S:292:HIS:H	2.21	0.44
1:S:1302:TRP:HH2	1:S:1348:ILE:HD13	1.80	0.44
10:U:395:PRO:HG2	10:U:455:PRO:HB2	1.99	0.44
11:V:676:PHE:CD2	11:V:680:VAL:HG21	2.51	0.44
11:V:752:ILE:O	11:V:754:GLY:N	2.50	0.44
11:V:1077:GLY:O	11:V:1083:ASN:ND2	2.46	0.44
11:V:1259:GLN:HG2	11:V:1260:ILE:H	1.82	0.44
1:A:769:LEU:HD21	1:A:784:LEU:HD22	1.99	0.44
2:B:73:HIS:CB	2:B:99:ASN:HB3	2.47	0.44
5:F:188:PHE:CZ	5:F:192:LEU:HD11	2.53	0.44
7:M:271:ILE:HD12	7:M:271:ILE:HA	1.89	0.44
7:M:337:CYS:O	7:M:340:GLU:HG3	2.17	0.44
2:O:344:LEU:HD11	2:O:354:LEU:HD12	2.00	0.44
2:O:477:LYS:HG3	2:O:478:ILE:H	1.82	0.44
8:P:255:LEU:O	8:P:256:LYS:C	2.54	0.44
8:P:335:VAL:HG13	8:P:336:PRO:HD2	2.00	0.44
8:P:648:ASP:O	8:P:650:LEU:N	2.45	0.44
1:S:981:CYS:HB3	1:S:1021:LEU:HD11	1.99	0.44
1:S:1053:ARG:HH11	1:S:1111:LEU:HD22	1.81	0.44
10:U:357:ARG:HH22	10:U:1101:TRP:HZ2	1.66	0.44
11:V:922:HIS:CD2	11:V:923:ALA:HB2	2.53	0.44
11:V:937:HIS:CD2	11:V:1023:MET:HG2	2.52	0.44
1:A:332:PRO:HB2	1:A:335:LYS:HE3	1.99	0.44
1:A:494:LEU:HD13	1:A:518:LEU:HD12	1.98	0.44
1:A:1322:VAL:HG13	1:A:1323:ALA:H	1.82	0.44
4:E:21:GLN:OE1	4:E:21:GLN:N	2.50	0.44
4:E:79:GLY:CA	7:L:73:ARG:HH22	2.31	0.44
5:F:112:VAL:HA	5:F:115:LEU:HD12	2.00	0.44
6:G:296:THR:O	6:G:300:LEU:HG	2.17	0.44
6:G:483:LEU:HD23	6:G:513:ARG:HA	1.98	0.44
2:O:685:ILE:HD13	2:O:691:VAL:HG23	2.00	0.44
8:Q:195:PRO:HB3	8:Q:246:PRO:HD3	1.98	0.44
8:Q:511:SER:HB2	8:Q:526:THR:OG1	2.17	0.44
1:S:456:PHE:CE1	1:S:496:PRO:HB2	2.52	0.44
1:S:776:LEU:HD23	1:S:781:VAL:HG12	2.00	0.44
1:S:780:HIS:NE2	9:W:88:THR:O	2.32	0.44
10:U:71:CYS:O	10:U:74:GLN:HG3	2.18	0.44
11:V:78:LYS:HD2	11:V:81:GLN:NE2	2.31	0.44
11:V:1227:THR:HG23	11:V:1230:THR:H	1.83	0.44
4:E:357:LEU:HD13	4:E:397:PRO:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:558:LEU:HD22	6:G:566:GLU:OE1	2.18	0.44
7:M:307:CYS:SG	7:M:334:HIS:N	2.91	0.44
2:O:624:LEU:HA	2:O:624:LEU:HD12	1.69	0.44
8:P:543:LEU:HD23	8:P:567:ILE:HD11	2.00	0.44
8:P:734:GLN:HE22	8:P:747:ARG:CB	2.30	0.44
8:Q:405:VAL:HG12	8:Q:407:LEU:HG	2.00	0.44
8:Q:589:ASN:ND2	8:Q:671:PRO:HB2	2.32	0.44
1:S:145:LEU:O	1:S:149:LEU:HD23	2.17	0.44
1:S:171:TRP:CZ2	1:S:196:LEU:HG	2.52	0.44
11:V:1292:HIS:CD2	11:V:1352:ARG:HG2	2.53	0.44
1:A:58:ASN:O	1:A:62:LEU:HG	2.17	0.44
1:A:179:LEU:HD11	1:A:238:PHE:CZ	2.53	0.44
1:A:1117:ARG:HB3	1:A:1165:LEU:HD21	1.99	0.44
2:B:673:LYS:HD3	2:B:673:LYS:N	2.31	0.44
3:C:246:HIS:CG	3:C:246:HIS:O	2.69	0.44
6:G:175:LYS:HD3	6:G:175:LYS:HA	1.52	0.44
6:G:232:LEU:HD12	6:G:248:VAL:HG13	1.99	0.44
6:H:214:ARG:HG2	6:H:330:PRO:HD3	1.99	0.44
7:M:15:LEU:HA	7:M:15:LEU:HD23	1.75	0.44
8:Q:226:GLY:HA2	8:Q:234:THR:OG1	2.18	0.44
10:U:154:GLU:OE2	10:U:155:GLU:HG2	2.18	0.44
10:U:496:VAL:HG12	10:U:500:LEU:HD12	2.00	0.44
10:U:505:PRO:HA	10:U:508:LYS:HG3	2.00	0.44
10:U:959:ILE:HG21	10:U:1006:MET:SD	2.57	0.44
10:U:1010:THR:CG2	10:U:1031:LEU:HD21	2.48	0.44
11:V:211:ILE:HG13	11:V:212:ILE:N	2.33	0.44
11:V:1354:THR:HA	11:V:1357:VAL:HG23	1.99	0.44
1:A:1209:ASP:O	1:A:1212:SER:OG	2.36	0.44
6:H:80:LEU:HD12	6:H:197:LEU:HD11	1.99	0.44
6:H:567:ALA:O	6:H:571:TRP:HD1	2.01	0.44
2:O:284:PRO:HA	2:O:303:PHE:HA	2.00	0.44
8:Q:602:LEU:HD23	8:Q:602:LEU:HA	1.91	0.44
1:S:153:GLN:O	1:S:156:LEU:HG	2.18	0.44
1:S:815:PRO:HB3	1:S:861:SER:HB3	2.00	0.44
1:S:853:ARG:HB3	1:S:855:THR:HG23	2.00	0.44
10:U:643:PRO:HB3	10:U:720:ASP:HB3	1.99	0.44
10:U:658:ILE:CD1	10:U:738:LYS:HE3	2.47	0.44
10:U:1251:PRO:HA	10:U:1254:ILE:HG12	1.99	0.44
1:A:284:GLY:O	1:A:286:GLN:NE2	2.51	0.44
1:A:386:TRP:CH2	1:A:429:THR:HG22	2.53	0.44
1:A:1079:LYS:O	1:A:1082:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1239:GLU:HA	1:A:1242:ILE:HD12	1.99	0.44
2:B:677:LEU:O	2:B:681:LYS:HA	2.18	0.44
4:E:290:ARG:HH12	4:E:312:GLU:HG3	1.83	0.44
5:F:266:ARG:HG3	5:F:267:HIS:CE1	2.53	0.44
6:H:353:ARG:O	6:H:357:THR:HG23	2.18	0.44
2:O:211:LYS:HB2	2:O:231:PRO:HB3	1.99	0.44
8:P:26:PRO:C	8:P:27:ARG:HG2	2.38	0.44
8:Q:498:SER:O	8:Q:499:SER:OG	2.34	0.44
8:Q:546:GLN:HG3	8:Q:599:SER:OG	2.18	0.44
8:Q:569:VAL:CG1	8:Q:572:LEU:HB2	2.47	0.44
8:Q:656:PRO:HG3	8:Q:757:VAL:HG23	2.00	0.44
8:Q:664:ARG:HD2	8:Q:664:ARG:N	2.33	0.44
1:S:948:ASP:O	1:S:951:ARG:HB2	2.18	0.44
1:S:1076:LEU:O	1:S:1080:ARG:HG2	2.17	0.44
1:S:1106:GLU:OE1	1:S:1106:GLU:N	2.49	0.44
10:U:439:GLU:HA	10:U:442:GLU:HG3	2.00	0.44
10:U:828:SER:O	10:U:831:VAL:HG22	2.17	0.44
11:V:215:LEU:N	11:V:216:PRO:HD3	2.33	0.44
11:V:343:ILE:O	11:V:346:LEU:HB3	2.17	0.44
11:V:1122:HIS:CB	11:V:1158:LEU:HD11	2.48	0.44
1:A:163:ARG:CZ	8:P:845:GLN:HE21	2.31	0.44
1:A:1331:LEU:N	1:A:1332:PRO:HD2	2.32	0.44
1:A:1339:LEU:HD11	1:A:1343:HIS:ND1	2.32	0.44
2:B:344:LEU:HD11	2:B:354:LEU:HA	1.99	0.44
3:C:197:ASP:N	3:C:198:PRO:HD2	2.33	0.44
4:E:438:LEU:O	4:E:442:LEU:HG	2.17	0.44
6:H:67:LEU:O	6:H:71:LEU:HD12	2.18	0.44
8:P:31:HIS:CD2	8:P:32:GLU:HG2	2.53	0.44
8:P:482:ALA:O	8:P:485:SER:OG	2.30	0.44
8:Q:325:LYS:O	8:Q:337:GLU:HG2	2.18	0.44
1:S:57:LEU:O	1:S:60:LEU:HB3	2.18	0.44
1:S:171:TRP:O	1:S:174:GLN:HB2	2.18	0.44
1:S:515:LYS:O	1:S:518:LEU:HB2	2.18	0.44
1:S:818:PHE:CB	1:S:864:LEU:HD21	2.47	0.44
1:S:1292:LEU:HD23	1:S:1295:LEU:HD12	2.00	0.44
10:U:416:GLN:NE2	10:U:420:LYS:HD2	2.33	0.44
10:U:605:LEU:HD12	10:U:609:PHE:CZ	2.53	0.44
10:U:739:ASN:HA	10:U:742:SER:OG	2.18	0.44
10:U:998:PRO:HA	10:U:1003:PHE:CG	2.53	0.44
10:U:1210:TYR:HA	10:U:1213:ILE:HD12	1.99	0.44
11:V:842:ASN:O	11:V:846:GLU:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:V:1094:LEU:HD22	11:V:1114:SER:HA	1.99	0.44
1:A:656:ALA:HB3	1:A:683:ARG:NH2	2.32	0.43
2:B:770:LEU:HD22	8:P:837:HIS:NE2	2.33	0.43
2:B:828:LEU:O	8:P:826:ARG:HA	2.18	0.43
3:C:153:MET:HA	5:F:161:SER:OG	2.18	0.43
6:G:174:SER:O	6:G:180:LEU:HD21	2.17	0.43
6:G:484:PHE:HB3	6:G:485:ARG:NH2	2.32	0.43
6:H:557:THR:HG22	6:H:560:ARG:NH1	2.32	0.43
6:H:562:ASP:N	6:H:562:ASP:OD1	2.50	0.43
7:L:293:PRO:HB2	7:L:296:ALA:HB2	2.00	0.43
7:M:55:CYS:HB3	7:M:59:LEU:HB3	2.00	0.43
7:M:320:PRO:HA	7:M:333:PHE:O	2.18	0.43
2:O:182:VAL:HA	2:O:215:TYR:O	2.17	0.43
8:P:227:LEU:HB2	8:P:334:LEU:CD2	2.48	0.43
8:Q:398:SER:HB2	8:Q:422:ALA:HB1	1.99	0.43
8:Q:529:LEU:CD2	8:Q:572:LEU:HD11	2.47	0.43
8:Q:737:LEU:HD11	8:Q:754:ILE:CD1	2.48	0.43
1:S:19:ARG:HA	1:S:19:ARG:NH1	2.33	0.43
1:S:163:ARG:CZ	1:S:191:VAL:HA	2.47	0.43
1:S:281:LEU:HD21	1:S:295:VAL:HG21	2.00	0.43
1:S:293:LYS:HA	1:S:296:ARG:HB2	2.00	0.43
1:S:452:PHE:O	1:S:455:SER:OG	2.26	0.43
1:S:557:VAL:HG11	1:S:1069:LEU:HD22	2.00	0.43
1:A:145:LEU:O	1:A:149:LEU:HD23	2.19	0.43
1:A:167:CYS:HB2	1:A:196:LEU:HD23	2.00	0.43
2:B:267:SER:OG	2:B:268:PHE:N	2.52	0.43
2:B:387:ARG:O	2:B:390:VAL:HG12	2.18	0.43
6:G:311:ASN:HA	6:G:343:GLN:OE1	2.18	0.43
2:O:604:ARG:HG3	2:O:605:GLU:N	2.33	0.43
8:P:152:MET:SD	8:P:253:VAL:HG11	2.58	0.43
1:S:1022:GLN:NE2	1:S:1084:ARG:O	2.51	0.43
1:S:1101:ILE:HG21	1:S:1154:PHE:HE2	1.81	0.43
11:V:202:ILE:HG13	11:V:203:ALA:N	2.33	0.43
11:V:338:SER:OG	11:V:339:GLY:N	2.51	0.43
11:V:1052:VAL:HG13	11:V:1053:GLN:OE1	2.17	0.43
1:A:1260:LEU:HD12	1:A:1261:PHE:N	2.33	0.43
2:B:573:GLU:HG3	2:B:574:CYS:O	2.18	0.43
2:B:710:ARG:HE	2:B:710:ARG:HB3	1.68	0.43
3:C:437:GLN:OE1	3:C:441:GLN:NE2	2.51	0.43
4:E:464:MET:HG3	4:E:468:LYS:HB2	2.00	0.43
6:H:275:GLU:OE1	6:H:275:GLU:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:100:LYS:O	2:O:100:LYS:HG2	2.18	0.43
8:P:241:VAL:O	8:P:252:CYS:HA	2.18	0.43
1:S:331:SER:O	1:S:331:SER:OG	2.33	0.43
1:A:1322:VAL:HG13	1:A:1323:ALA:N	2.33	0.43
2:B:79:CYS:HB3	2:B:94:ILE:HD13	2.00	0.43
3:C:496:LEU:O	3:C:543:SER:OG	2.26	0.43
4:E:67:LEU:HD23	4:E:67:LEU:HA	1.75	0.43
4:E:80:ARG:NH2	4:E:82:GLU:HG2	2.34	0.43
6:H:78:ILE:HG23	6:H:92:GLN:HG2	2.00	0.43
6:H:397:PHE:CB	6:H:420:LEU:HD22	2.49	0.43
7:L:152:LEU:HD12	7:L:152:LEU:N	2.33	0.43
8:P:169:GLN:O	8:P:169:GLN:HG2	2.17	0.43
8:Q:289:LYS:HA	8:Q:310:ASP:H	1.84	0.43
1:S:1313:LEU:HD13	1:S:1317:ARG:HG3	2.00	0.43
10:U:1036:HIS:CE1	10:U:1045:LEU:HD13	2.53	0.43
11:V:190:LYS:H	11:V:190:LYS:HE2	1.83	0.43
11:V:364:TRP:NE1	11:V:384:MET:HG2	2.33	0.43
11:V:1273:ARG:O	11:V:1277:ILE:HG12	2.18	0.43
1:A:667:PRO:HA	1:A:673:ILE:HD11	2.00	0.43
6:G:141:ARG:CG	6:G:200:ALA:HB2	2.49	0.43
6:G:453:SER:HB2	6:G:483:LEU:CD1	2.48	0.43
6:G:551:TYR:CD2	6:G:574:LEU:HD21	2.53	0.43
6:H:149:LEU:O	6:H:152:SER:OG	2.27	0.43
7:L:191:LEU:HD23	7:L:191:LEU:HA	1.79	0.43
8:P:504:ARG:N	8:P:505:PRO:HD3	2.33	0.43
8:P:677:ALA:O	8:P:680:LEU:HG	2.19	0.43
8:Q:331:SER:OG	8:Q:333:LYS:HG2	2.18	0.43
8:Q:880:LEU:O	8:Q:881:LEU:HD12	2.18	0.43
1:S:93:PHE:O	1:S:96:SER:OG	2.31	0.43
1:S:795:ARG:HD3	1:S:814:VAL:HG23	2.01	0.43
1:S:952:GLN:HA	1:S:955:HIS:HB2	2.00	0.43
1:S:1126:LEU:HB3	1:S:1130:ILE:HD11	2.00	0.43
10:U:29:LEU:HD13	10:U:71:CYS:SG	2.59	0.43
10:U:805:LEU:HD22	10:U:809:PHE:CE2	2.54	0.43
1:A:1126:LEU:HD13	1:A:1169:SER:HB3	2.01	0.43
3:C:529:THR:HA	3:C:532:ARG:NH2	2.33	0.43
6:G:140:HIS:CE1	6:G:166:LEU:HD21	2.54	0.43
6:G:213:TYR:CD2	6:G:329:LEU:HD22	2.54	0.43
6:G:433:ARG:HG3	6:G:446:PRO:HG3	2.01	0.43
6:H:203:LEU:O	6:H:207:LEU:HG	2.18	0.43
7:L:250:GLU:N	7:L:250:GLU:OE1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:37:HIS:CD2	7:M:38:LEU:H	2.37	0.43
7:M:107:PRO:N	7:M:108:PRO:CD	2.81	0.43
2:O:601:ILE:HG22	2:O:611:LYS:HZ2	1.83	0.43
8:Q:60:PHE:CE1	8:Q:118:VAL:HG21	2.53	0.43
1:S:171:TRP:CE2	1:S:200:HIS:HB2	2.54	0.43
1:S:324:LEU:HD21	1:S:362:LEU:HD22	2.00	0.43
10:U:365:LEU:HB3	10:U:369:LYS:HZ1	1.83	0.43
10:U:998:PRO:HA	10:U:1003:PHE:CD2	2.53	0.43
11:V:92:ILE:O	11:V:96:PHE:HB2	2.19	0.43
11:V:258:PHE:O	11:V:262:VAL:HG23	2.18	0.43
11:V:659:ASP:HB3	11:V:733:TYR:OH	2.19	0.43
11:V:1186:LEU:HD11	11:V:1234:PHE:CE1	2.54	0.43
2:B:112:LEU:HD12	2:B:118:PHE:CZ	2.54	0.43
3:C:187:CYS:HG	3:C:219:PHE:HE1	1.63	0.43
3:C:224:ASN:ND2	3:C:249:SER:OG	2.51	0.43
4:E:298:LEU:HD11	4:E:347:TRP:CZ3	2.53	0.43
6:H:351:ALA:HB1	6:H:367:TYR:CD2	2.54	0.43
8:P:147:PRO:O	8:P:149:ARG:N	2.52	0.43
8:P:760:ASP:OD1	8:P:760:ASP:N	2.45	0.43
1:S:346:TRP:CE3	1:S:387:GLN:HA	2.54	0.43
1:S:763:THR:HB	9:W:101:UNK:HA	1.99	0.43
1:S:842:SER:O	1:S:845:LEU:HG	2.19	0.43
1:S:1118:ASN:O	1:S:1326:GLN:NE2	2.51	0.43
10:U:501:LYS:HB3	10:U:501:LYS:HE2	1.72	0.43
10:U:852:GLN:OE1	10:U:860:SER:HB3	2.18	0.43
10:U:860:SER:OG	10:U:861:GLY:N	2.51	0.43
11:V:754:GLY:HA2	11:V:757:ASP:OD2	2.18	0.43
11:V:1357:VAL:O	11:V:1361:LYS:HG2	2.19	0.43
1:A:455:SER:O	1:A:460:ARG:N	2.38	0.43
1:A:468:LYS:HA	1:A:471:VAL:CG2	2.46	0.43
3:C:306:ASP:O	4:E:176:ARG:HB2	2.19	0.43
5:F:43:HIS:HE1	5:F:47:ARG:HH21	1.67	0.43
6:G:597:LEU:HB3	6:G:601:ARG:HH21	1.83	0.43
6:H:555:LEU:O	6:H:559:LYS:HG2	2.19	0.43
6:H:569:ALA:O	6:H:573:ARG:HG2	2.19	0.43
7:L:228:ILE:HD12	7:L:238:ILE:HD12	1.99	0.43
2:O:260:THR:OG1	2:O:264:GLN:HB2	2.18	0.43
8:P:133:PHE:O	8:P:133:PHE:CG	2.65	0.43
8:P:195:PRO:HB3	8:P:246:PRO:HD3	2.00	0.43
8:P:875:HIS:HB3	8:P:876:PRO:CD	2.48	0.43
8:Q:289:LYS:HD3	8:Q:308:HIS:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Q:604:TYR:HB3	8:Q:638:VAL:CG1	2.49	0.43
1:S:795:ARG:HD2	1:S:813:PRO:HB3	1.99	0.43
10:U:288:GLU:OE1	10:U:288:GLU:HA	2.19	0.43
10:U:595:LEU:HD11	10:U:626:THR:HG22	1.99	0.43
10:U:1059:ASP:OD1	10:U:1060:ILE:N	2.51	0.43
11:V:359:THR:HA	11:V:362:GLU:OE1	2.19	0.43
11:V:364:TRP:CZ2	11:V:380:PHE:HE1	2.36	0.43
11:V:647:LYS:HA	11:V:650:GLU:HG3	2.01	0.43
11:V:668:SER:OG	11:V:693:ASP:O	2.27	0.43
1:A:825:ARG:HB3	1:A:940:GLN:HG3	1.99	0.43
2:B:619:ARG:HH22	8:P:635:GLN:HG2	1.84	0.43
3:C:115:GLN:CD	5:F:108:ARG:HD2	2.38	0.43
3:C:162:ARG:NH1	3:C:162:ARG:O	2.51	0.43
3:C:339:THR:O	3:C:339:THR:CG2	2.67	0.43
4:E:415:ALA:O	4:E:419:LEU:HD23	2.19	0.43
6:G:256:HIS:NE2	6:G:268:TYR:HE2	2.17	0.43
7:M:132:CYS:SG	7:M:134:SER:HB3	2.59	0.43
2:O:723:ASN:OD1	2:O:726:VAL:HG23	2.19	0.43
8:P:283:ILE:O	8:P:283:ILE:HG22	2.16	0.43
8:Q:286:GLY:O	8:Q:312:LEU:HD12	2.18	0.43
1:S:732:ALA:HB1	9:W:79:THR:HG21	2.01	0.43
1:S:992:HIS:O	1:S:1073:ARG:NH2	2.52	0.43
1:S:1020:ARG:O	1:S:1024:MET:HG2	2.19	0.43
1:S:1292:LEU:HD23	1:S:1292:LEU:HA	1.82	0.43
10:U:1029:MET:HE3	10:U:1084:VAL:HG13	2.01	0.43
11:V:190:LYS:N	11:V:190:LYS:HD3	2.34	0.43
11:V:527:GLN:HA	11:V:530:ARG:HH12	1.83	0.43
11:V:656:ILE:HG21	11:V:736:LEU:HD22	1.99	0.43
11:V:969:LEU:HD13	11:V:1065:LEU:HG	2.01	0.43
11:V:972:LEU:HD12	11:V:976:LEU:HD13	2.01	0.43
11:V:1115:VAL:HG21	11:V:1142:LEU:CG	2.48	0.43
1:A:426:SER:O	1:A:429:THR:OG1	2.37	0.43
1:A:1135:PHE:HA	1:A:1138:LEU:HD12	2.01	0.43
4:E:101:LEU:O	4:E:105:VAL:HG22	2.19	0.43
6:G:447:TYR:HA	6:G:487:THR:O	2.19	0.43
6:H:373:LEU:HD12	6:H:374:LEU:HG	2.01	0.43
6:H:545:PRO:HB2	6:H:577:GLN:OE1	2.19	0.43
7:M:210:LYS:O	7:M:210:LYS:HD3	2.19	0.43
2:O:83:SER:HB2	2:O:90:ASN:HA	2.01	0.43
2:O:250:ASN:OD1	2:O:251:GLN:HG3	2.19	0.43
2:O:485:ASP:O	2:O:583:SER:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Q:258:LEU:O	8:Q:258:LEU:HD23	2.19	0.43
8:Q:655:PHE:HA	8:Q:756:GLY:CA	2.49	0.43
8:Q:709:LYS:HG2	8:Q:786:GLU:HB3	2.00	0.43
10:U:707:GLU:O	10:U:710:THR:OG1	2.32	0.43
10:U:757:ASN:ND2	10:U:767:ARG:O	2.52	0.43
11:V:787:PHE:CZ	11:V:924:PHE:HB3	2.54	0.43
1:A:1115:GLU:HB2	1:A:1116:MET:HE1	2.00	0.42
4:E:53:ARG:NH2	7:L:361:TYR:O	2.52	0.42
4:E:420:LEU:HD23	4:E:423:LEU:HD12	2.00	0.42
6:G:191:LEU:O	6:G:193:ALA:N	2.52	0.42
6:H:155:ARG:O	6:H:158:ASP:OD1	2.37	0.42
2:O:425:ALA:O	2:O:429:LEU:HG	2.18	0.42
2:O:781:GLU:HG2	8:Q:826:ARG:HG2	2.00	0.42
8:P:142:THR:OG1	8:P:143:LEU:N	2.52	0.42
8:P:325:LYS:HG2	8:P:326:ALA:N	2.34	0.42
8:Q:655:PHE:CD1	8:Q:756:GLY:HA3	2.54	0.42
1:S:21:ALA:HA	1:S:24:GLU:HB2	2.01	0.42
10:U:747:MET:HG2	10:U:778:TYR:HD1	1.83	0.42
11:V:190:LYS:H	11:V:190:LYS:HD3	1.83	0.42
11:V:306:ASP:CG	11:V:307:LEU:N	2.72	0.42
11:V:1331:PHE:HA	11:V:1334:ASP:OD2	2.19	0.42
1:A:34:LYS:HE3	6:H:313:PRO:HD3	2.02	0.42
1:A:346:TRP:CE2	1:A:387:GLN:HA	2.55	0.42
1:A:369:GLU:HA	1:A:372:VAL:HG22	2.00	0.42
3:C:302:LEU:HD12	3:C:302:LEU:HA	1.82	0.42
3:C:379:VAL:HG21	3:C:428:PHE:CZ	2.54	0.42
7:M:29:ILE:HD12	7:M:30:SER:H	1.84	0.42
2:O:297:LEU:HD13	2:O:313:LYS:HD3	2.01	0.42
2:O:507:SER:OG	8:Q:564:THR:HG21	2.19	0.42
8:P:744:ASP:OD1	8:P:744:ASP:N	2.51	0.42
8:Q:60:PHE:HE2	8:Q:78:ALA:CB	2.32	0.42
1:S:45:GLU:O	1:S:48:VAL:HG12	2.18	0.42
1:S:1135:PHE:CD2	1:S:1177:LEU:HD13	2.54	0.42
10:U:364:ILE:O	10:U:368:VAL:HG23	2.19	0.42
10:U:541:LEU:HD22	10:U:608:GLY:HA3	2.00	0.42
11:V:391:THR:OG1	11:V:392:ASN:N	2.51	0.42
1:A:43:LEU:HD23	1:A:44:LYS:N	2.34	0.42
1:A:288:GLU:HG3	1:A:292:HIS:CD2	2.54	0.42
2:B:281:PHE:N	2:B:281:PHE:CD1	2.87	0.42
5:F:339:PHE:CG	5:F:344:LEU:HD22	2.54	0.42
6:H:600:ILE:O	6:H:600:ILE:HG22	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:501:LEU:O	2:O:604:ARG:HG2	2.18	0.42
2:O:656:HIS:CD2	2:O:657:LYS:N	2.87	0.42
8:P:545:ILE:CD1	8:P:565:TYR:HB2	2.48	0.42
8:Q:21:LEU:HB2	8:Q:399:LEU:CD2	2.47	0.42
11:V:83:LEU:HG	11:V:92:ILE:HD12	2.01	0.42
11:V:140:LEU:HD23	11:V:146:GLN:HA	2.00	0.42
1:A:1289:ALA:O	1:A:1292:LEU:HG	2.19	0.42
2:B:99:ASN:ND2	2:B:101:LYS:H	2.17	0.42
2:B:280:PRO:HB2	2:B:281:PHE:CD1	2.54	0.42
7:L:336:ILE:H	7:L:336:ILE:HD12	1.84	0.42
8:P:859:SER:OG	8:P:860:CYS:N	2.53	0.42
1:S:229:ASP:O	1:S:232:ARG:HG2	2.19	0.42
1:S:814:VAL:N	1:S:815:PRO:HD2	2.34	0.42
10:U:613:LEU:HD21	10:U:620:ALA:HA	2.01	0.42
10:U:721:PHE:HB2	10:U:723:LEU:HG	2.01	0.42
10:U:1135:ILE:HD11	10:U:1194:MET:HA	2.00	0.42
11:V:51:LEU:HD13	11:V:83:LEU:HD11	2.02	0.42
1:A:332:PRO:HB3	1:A:383:GLU:OE1	2.19	0.42
1:A:415:MET:CE	1:A:415:MET:HA	2.49	0.42
1:A:456:PHE:CE2	1:A:496:PRO:HB2	2.55	0.42
1:A:1193:LEU:HD12	1:A:1194:PRO:HD2	2.01	0.42
2:B:506:LEU:N	2:B:525:ASN:HD21	2.09	0.42
3:C:291:PHE:CE2	3:C:340:TYR:HB3	2.55	0.42
4:E:113:GLY:O	4:E:116:SER:OG	2.31	0.42
4:E:129:PRO:HG3	4:E:134:ARG:HH12	1.84	0.42
6:G:559:LYS:HA	6:G:563:ARG:HG2	2.02	0.42
6:H:455:THR:O	6:H:458:LEU:HG	2.19	0.42
1:S:1336:TYR:OH	1:S:1361:TYR:N	2.53	0.42
10:U:131:PRO:HD3	10:U:180:MET:HG3	2.01	0.42
10:U:488:LEU:HD21	10:U:500:LEU:HD11	2.00	0.42
11:V:337:SER:N	11:V:340:GLN:OE1	2.53	0.42
11:V:783:CYS:SG	11:V:784:SER:N	2.92	0.42
1:A:1028:LEU:HD13	1:A:1047:PHE:CE2	2.55	0.42
2:B:766:GLU:O	2:B:769:THR:OG1	2.34	0.42
6:G:89:THR:HG21	8:P:147:PRO:CB	2.49	0.42
6:G:598:SER:HA	6:G:601:ARG:CZ	2.49	0.42
6:H:461:GLN:HG2	6:H:596:TYR:CE1	2.54	0.42
7:L:55:CYS:HB3	7:L:59:LEU:HB3	2.02	0.42
2:O:630:GLY:O	2:O:631:LYS:HB3	2.19	0.42
8:P:395:CYS:HB3	8:P:396:PRO:CD	2.49	0.42
8:P:508:CYS:SG	8:P:642:LEU:HD13	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Q:239:PRO:HG2	8:Q:255:LEU:HD12	2.00	0.42
8:Q:505:PRO:CB	8:Q:533:SER:HB3	2.50	0.42
8:Q:720:LYS:C	8:Q:722:GLY:N	2.70	0.42
1:S:266:THR:O	1:S:270:LEU:HG	2.20	0.42
1:S:303:SER:O	1:S:305:HIS:ND1	2.52	0.42
1:S:822:LEU:HG	1:S:833:CYS:SG	2.60	0.42
1:S:1090:LEU:HD12	1:S:1091:CYS:N	2.35	0.42
10:U:770:ASP:O	10:U:773:SER:OG	2.32	0.42
10:U:868:GLU:OE1	10:U:926:LYS:NZ	2.53	0.42
10:U:979:SER:O	10:U:983:LEU:HG	2.19	0.42
10:U:1096:LEU:HA	10:U:1099:VAL:HG22	2.02	0.42
10:U:1137:GLN:O	10:U:1141:LEU:HD12	2.20	0.42
11:V:299:SER:O	11:V:303:GLU:HG2	2.20	0.42
11:V:922:HIS:CG	11:V:923:ALA:N	2.88	0.42
1:A:657:LEU:HD23	1:A:657:LEU:HA	1.89	0.42
1:A:988:LEU:HD11	1:A:1081:ILE:HD11	2.02	0.42
2:B:65:PHE:HE2	2:B:67:ILE:HD13	1.84	0.42
2:B:391:VAL:O	2:B:394:LEU:N	2.52	0.42
2:B:394:LEU:HD11	7:L:115:ILE:HD11	2.02	0.42
3:C:25:ALA:HA	3:C:30:THR:OG1	2.20	0.42
3:C:31:GLN:OE1	3:C:185:ARG:NE	2.46	0.42
3:C:166:LEU:HA	3:C:166:LEU:HD23	1.79	0.42
3:C:359:ILE:HD12	3:C:403:TRP:HH2	1.84	0.42
5:F:282:GLY:HA3	5:F:347:TRP:CH2	2.55	0.42
2:O:842:VAL:HG12	8:Q:878:LEU:HD21	2.01	0.42
8:P:23:ALA:HA	8:P:399:LEU:HD12	2.01	0.42
8:Q:76:LEU:HD23	8:Q:76:LEU:HA	1.87	0.42
1:S:108:PRO:HG2	1:S:111:ILE:HD12	2.02	0.42
1:S:605:GLU:HA	1:S:608:LYS:HG2	2.01	0.42
1:S:874:ARG:HG3	1:S:946:LEU:HD11	2.00	0.42
10:U:593:ARG:CD	11:V:182:TRP:HZ3	2.33	0.42
10:U:672:GLN:HG3	10:U:756:TYR:HB2	2.02	0.42
10:U:768:PHE:HE2	10:U:828:SER:HG	1.65	0.42
11:V:215:LEU:N	11:V:216:PRO:CD	2.83	0.42
11:V:607:CYS:HA	11:V:610:VAL:HG12	2.01	0.42
11:V:1008:SER:O	11:V:1012:ILE:HG12	2.20	0.42
1:A:822:LEU:CD2	1:A:867:LYS:HD3	2.49	0.42
3:C:251:GLU:O	3:C:255:LEU:HG	2.20	0.42
4:E:399:CYS:SG	4:E:400:SER:N	2.92	0.42
5:F:115:LEU:HD23	5:F:129:LEU:CD2	2.46	0.42
6:G:273:LEU:CD2	6:G:279:TRP:HB2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:168:GLY:HA3	6:H:170:GLN:NE2	2.34	0.42
6:H:539:LEU:O	6:H:543:MET:HG2	2.20	0.42
7:M:248:LEU:HD21	10:U:472:LEU:HD11	2.00	0.42
7:M:326:ASN:ND2	7:M:364:LYS:HG3	2.35	0.42
8:Q:524:MET:SD	8:Q:583:PRO:HB3	2.59	0.42
1:S:149:LEU:CD1	1:S:190:ILE:HG13	2.49	0.42
1:S:393:VAL:HA	1:S:396:LEU:HB2	2.01	0.42
1:S:814:VAL:HG12	1:S:818:PHE:CE2	2.54	0.42
10:U:298:GLN:HE22	10:U:1108:GLY:HA3	1.84	0.42
10:U:593:ARG:CD	11:V:182:TRP:CZ3	3.03	0.42
10:U:612:VAL:O	10:U:616:ASN:N	2.47	0.42
10:U:968:ASN:OD1	10:U:969:LEU:N	2.52	0.42
11:V:298:ILE:HG21	11:V:364:TRP:HA	2.02	0.42
11:V:527:GLN:HA	11:V:530:ARG:NH1	2.34	0.42
11:V:647:LYS:HA	11:V:650:GLU:CG	2.49	0.42
11:V:686:LEU:HD23	11:V:686:LEU:HA	1.86	0.42
11:V:1227:THR:O	11:V:1231:PHE:HB2	2.19	0.42
11:V:1277:ILE:O	11:V:1281:LEU:HD13	2.20	0.42
1:A:495:HIS:HB3	1:A:496:PRO:HD3	2.01	0.42
1:A:663:SER:HB3	1:A:676:GLN:HE22	1.85	0.42
1:A:1362:LEU:HD12	1:A:1363:LYS:N	2.35	0.42
1:A:1368:PHE:CD2	1:A:1392:PRO:HB2	2.55	0.42
2:B:488:VAL:HG21	2:B:654:ALA:HB2	2.02	0.42
4:E:133:LEU:HD12	4:E:133:LEU:HA	1.80	0.42
5:F:11:PHE:CZ	5:F:89:CYS:HB2	2.54	0.42
5:F:14:LEU:HD11	5:F:26:TRP:CH2	2.55	0.42
5:F:69:GLU:HA	5:F:74:ARG:HH22	1.84	0.42
6:G:430:LYS:CE	8:P:328:TRP:HB2	2.50	0.42
6:G:522:LEU:HD21	6:G:553:HIS:CE1	2.55	0.42
6:H:37:LEU:O	6:H:40:GLN:HG3	2.18	0.42
7:L:226:ARG:HD3	7:L:226:ARG:HA	1.82	0.42
2:O:303:PHE:HB2	2:O:307:ASN:OD1	2.20	0.42
2:O:777:ILE:O	2:O:781:GLU:HG3	2.20	0.42
8:P:393:MET:CE	8:P:434:LEU:HD21	2.50	0.42
8:Q:563:ILE:HG22	8:Q:565:TYR:CE1	2.55	0.42
8:Q:736:LEU:HD23	8:Q:807:ARG:HH21	1.85	0.42
1:S:929:TYR:CE2	1:S:933:LEU:HD11	2.55	0.42
1:S:1331:LEU:N	1:S:1332:PRO:HD2	2.35	0.42
1:S:1398:LYS:HA	1:S:1401:LEU:HG	2.01	0.42
10:U:186:LEU:HD22	10:U:190:GLU:HB3	2.02	0.42
10:U:277:PHE:O	10:U:281:LEU:HG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:U:283:TYR:CD1	10:U:321:ARG:HD3	2.54	0.42
10:U:295:VAL:HG13	10:U:296:GLY:H	1.85	0.42
10:U:831:VAL:O	10:U:834:SER:OG	2.36	0.42
11:V:46:SER:OG	11:V:49:VAL:HG12	2.20	0.42
11:V:682:ALA:HB2	11:V:761:PHE:CE1	2.55	0.42
11:V:686:LEU:HG	11:V:815:ARG:CZ	2.50	0.42
11:V:767:PRO:HA	11:V:828:LYS:NZ	2.35	0.42
11:V:807:GLU:HG2	11:V:808:MET:N	2.35	0.42
11:V:814:THR:HA	11:V:817:LYS:HG2	2.02	0.42
1:A:61:LEU:HD12	1:A:77:VAL:HG22	2.02	0.42
1:A:342:MET:HB3	1:A:346:TRP:CE2	2.55	0.42
1:A:485:SER:O	1:A:485:SER:OG	2.29	0.42
1:A:914:ARG:O	1:A:917:ARG:N	2.53	0.42
2:B:15:LEU:HB2	2:B:327:LEU:HD13	2.02	0.42
3:C:72:ALA:HB2	3:C:113:TRP:HZ2	1.85	0.42
3:C:188:VAL:HB	3:C:189:PRO:HD3	2.02	0.42
6:G:256:HIS:HA	6:G:259:MET:CG	2.50	0.42
6:H:397:PHE:HB2	6:H:420:LEU:HD22	2.00	0.42
7:M:84:MET:C	7:M:88:LYS:HZ3	2.23	0.42
7:M:257:ASP:OD1	7:M:258:HIS:N	2.53	0.42
2:O:480:TYR:CZ	2:O:620:VAL:HG23	2.54	0.42
1:S:411:VAL:O	1:S:415:MET:HG3	2.20	0.42
1:S:944:ASP:OD1	1:S:947:SER:HA	2.20	0.42
1:S:1174:TRP:CD2	1:S:1200:LEU:HD22	2.55	0.42
1:S:1339:LEU:HD11	1:S:1343:HIS:ND1	2.35	0.42
10:U:106:VAL:HG22	10:U:137:LEU:HD21	2.02	0.42
10:U:239:ALA:O	10:U:243:GLN:HG2	2.20	0.42
10:U:310:ILE:O	10:U:314:LEU:HD23	2.20	0.42
11:V:190:LYS:H	11:V:190:LYS:CE	2.33	0.42
1:A:795:ARG:HG2	1:A:796:SER:N	2.35	0.41
1:A:818:PHE:HE1	1:A:836:PHE:HE2	1.66	0.41
1:A:1194:PRO:HG2	1:A:1197:LEU:HD13	2.02	0.41
2:B:106:GLU:O	2:B:107:TYR:HB2	2.20	0.41
2:B:402:PHE:O	2:B:405:PHE:HB3	2.21	0.41
3:C:232:ILE:HG23	3:C:233:SER:N	2.35	0.41
4:E:298:LEU:HD21	4:E:347:TRP:CZ2	2.54	0.41
6:G:374:LEU:HD13	6:G:393:MET:HE1	2.01	0.41
7:M:16:LEU:HD11	2:O:422:SER:CB	2.50	0.41
7:M:226:ARG:O	7:M:238:ILE:HG12	2.19	0.41
2:O:41:PRO:HB2	2:O:74:LEU:HD12	2.02	0.41
2:O:675:TRP:CH2	2:O:734:LEU:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:P:258:LEU:HD13	8:P:271:LEU:HD21	2.01	0.41
8:P:531:ASN:HB2	8:P:572:LEU:HD21	2.01	0.41
8:Q:165:ARG:HE	8:Q:166:PRO:CD	2.33	0.41
8:Q:280:GLU:OE2	8:Q:319:GLY:N	2.50	0.41
1:S:485:SER:HB2	1:S:521:LEU:HD13	2.02	0.41
1:S:660:LEU:HD12	1:S:660:LEU:HA	1.91	0.41
1:S:769:LEU:HD21	1:S:784:LEU:HD23	2.02	0.41
1:S:851:GLN:HG2	1:S:853:ARG:HH21	1.85	0.41
1:S:1326:GLN:HG2	1:S:1327:HIS:CD2	2.54	0.41
10:U:202:PHE:CD1	10:U:210:ILE:HG23	2.55	0.41
10:U:295:VAL:HG13	10:U:296:GLY:N	2.35	0.41
10:U:1102:LEU:HB3	10:U:1134:ILE:HD11	2.01	0.41
11:V:378:LYS:HE3	11:V:378:LYS:HB3	1.86	0.41
1:A:167:CYS:SG	1:A:168:GLN:N	2.93	0.41
2:B:657:LYS:HD2	2:B:720:TYR:CZ	2.55	0.41
3:C:303:LEU:HD21	3:C:391:PHE:CZ	2.55	0.41
2:O:13:GLU:HG3	2:O:353:CYS:SG	2.60	0.41
2:O:604:ARG:HH12	8:Q:551:SER:C	2.24	0.41
1:S:563:ASN:ND2	1:S:1275:SER:OG	2.53	0.41
1:S:1053:ARG:HA	1:S:1056:LEU:HD12	2.02	0.41
1:S:1109:PHE:HB3	1:S:1163:CYS:HB2	2.01	0.41
1:S:1262:PHE:CE2	1:S:1319:LEU:HD22	2.55	0.41
1:S:1404:LEU:HD21	1:S:1432:VAL:HG12	2.02	0.41
10:U:40:GLY:HA3	10:U:85:ILE:HG21	2.02	0.41
10:U:678:TYR:HA	10:U:682:VAL:HG23	2.02	0.41
10:U:1136:MET:CE	10:U:1193:ASN:HD21	2.33	0.41
11:V:171:ASN:OD1	11:V:171:ASN:N	2.50	0.41
11:V:212:ILE:HG13	11:V:215:LEU:HD12	2.02	0.41
11:V:456:LEU:HD12	11:V:460:TYR:HE2	1.84	0.41
11:V:787:PHE:CE1	11:V:924:PHE:HB3	2.55	0.41
1:A:60:LEU:O	1:A:64:VAL:HG22	2.21	0.41
1:A:278:LEU:HD11	1:A:327:ILE:HG12	2.03	0.41
1:A:1416:SER:HG	1:A:1417:HIS:HD1	1.53	0.41
2:B:14:ARG:HD2	2:B:79:CYS:SG	2.60	0.41
3:C:216:GLN:HA	3:C:217:PRO:HD3	1.87	0.41
3:C:343:TYR:HD1	3:C:344:THR:HG23	1.85	0.41
6:H:198:GLN:OE1	6:H:323:ILE:HB	2.20	0.41
6:H:551:TYR:HE1	6:H:570:LEU:HD22	1.84	0.41
2:O:132:ASP:HB2	2:O:145:ARG:O	2.19	0.41
2:O:216:SER:HB2	2:O:220:GLN:HB2	2.01	0.41
8:P:250:LEU:O	8:P:250:LEU:HG	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:P:467:GLU:C	8:P:470:SER:HG	2.14	0.41
8:Q:165:ARG:HE	8:Q:166:PRO:HD3	1.85	0.41
1:S:1128:GLN:HB2	1:S:1173:TRP:CE3	2.55	0.41
1:S:1261:PHE:CE1	1:S:1265:LEU:HD21	2.56	0.41
10:U:81:LEU:HB2	10:U:86:VAL:HG23	2.01	0.41
10:U:591:LEU:HA	10:U:594:CYS:SG	2.60	0.41
10:U:1019:ARG:HD2	10:U:1019:ARG:HA	1.89	0.41
10:U:1029:MET:HE2	10:U:1087:LEU:HD23	2.02	0.41
10:U:1146:HIS:O	10:U:1150:GLN:HG3	2.20	0.41
11:V:397:LYS:HB3	11:V:401:ARG:HH12	1.84	0.41
11:V:769:GLU:HA	11:V:772:GLU:HG2	2.01	0.41
3:C:247:LEU:HB2	4:E:132:TRP:CD1	2.56	0.41
5:F:341:VAL:O	5:F:344:LEU:HD13	2.20	0.41
7:L:63:LEU:HD23	7:L:63:LEU:HA	1.77	0.41
7:M:227:ARG:HA	7:M:237:ASN:HA	2.02	0.41
2:O:354:LEU:HG	2:O:354:LEU:O	2.21	0.41
2:O:523:CYS:HA	2:O:581:VAL:O	2.19	0.41
8:P:38:SER:O	8:P:38:SER:OG	2.39	0.41
8:Q:736:LEU:HD23	8:Q:807:ARG:NH2	2.35	0.41
1:S:153:GLN:NE2	1:S:188:GLN:HB3	2.35	0.41
1:S:481:VAL:O	1:S:485:SER:HB3	2.19	0.41
1:S:1349:ARG:HA	1:S:1353:PHE:CG	2.55	0.41
10:U:72:CYS:SG	10:U:93:LEU:HD11	2.60	0.41
10:U:197:LYS:O	10:U:201:MET:HG2	2.20	0.41
10:U:879:ARG:HH12	10:U:933:ALA:HB1	1.84	0.41
10:U:1180:TYR:HB3	10:U:1267:LEU:HD11	2.01	0.41
11:V:178:SER:OG	11:V:179:GLN:NE2	2.53	0.41
11:V:190:LYS:O	11:V:194:THR:HG23	2.20	0.41
1:A:758:LEU:O	1:A:762:LEU:HG	2.21	0.41
1:A:937:LEU:HA	1:A:1014:ASN:OD1	2.20	0.41
2:B:421:LYS:HE3	2:B:421:LYS:HB2	1.93	0.41
3:C:19:LEU:HD23	3:C:22:TRP:CE3	2.55	0.41
3:C:456:MET:O	3:C:459:SER:OG	2.29	0.41
4:E:288:LEU:N	4:E:289:PRO:HD2	2.36	0.41
4:E:442:LEU:O	4:E:475:LYS:NZ	2.23	0.41
6:G:21:ASP:OD1	6:G:195:LEU:HD23	2.20	0.41
6:G:54:LEU:HD21	6:G:58:GLN:NE2	2.36	0.41
6:G:151:LEU:HD21	6:G:214:ARG:HD3	2.02	0.41
6:G:501:GLN:HG3	6:G:502:GLY:N	2.35	0.41
6:H:88:PHE:CD1	6:H:149:LEU:HD23	2.55	0.41
7:L:126:LEU:HA	7:L:138:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:295:ARG:HD2	7:L:298:LEU:CD2	2.46	0.41
2:O:765:LYS:NZ	2:O:848:LYS:HB2	2.36	0.41
8:P:543:LEU:HD12	8:P:601:THR:O	2.20	0.41
8:Q:148:ALA:O	8:Q:180:PRO:HD2	2.20	0.41
8:Q:539:GLN:OE1	8:Q:609:VAL:HG22	2.20	0.41
1:S:114:ALA:HB1	1:S:166:PHE:HA	2.02	0.41
1:S:564:ILE:HD12	1:S:607:LEU:HD23	2.02	0.41
1:S:1437:GLN:O	1:S:1441:GLN:HG2	2.20	0.41
9:W:83:LYS:HE3	9:W:85:PHE:HZ	1.86	0.41
10:U:412:ARG:HD2	10:U:413:MET:N	2.35	0.41
10:U:950:SER:OG	10:U:951:VAL:N	2.52	0.41
11:V:283:LYS:HG3	11:V:287:HIS:CE1	2.55	0.41
2:B:229:ILE:HD12	2:B:237:VAL:HG21	2.03	0.41
5:F:193:TRP:CH2	5:F:198:GLN:HB3	2.56	0.41
7:L:117:GLU:OE1	7:L:158:TYR:OH	2.13	0.41
7:L:171:VAL:HG22	7:L:197:LEU:HD11	2.01	0.41
2:O:126:LEU:HD23	2:O:126:LEU:HA	1.90	0.41
8:P:17:PRO:HD2	8:P:21:LEU:HD23	2.02	0.41
8:P:150:TRP:CD2	8:P:178:TYR:CE2	3.08	0.41
8:P:328:TRP:HA	8:P:334:LEU:HA	2.02	0.41
1:S:169:GLU:HG3	1:S:172:LYS:HD2	2.03	0.41
1:S:316:LEU:HG	1:S:320:PHE:CE2	2.55	0.41
1:S:1080:ARG:HA	1:S:1080:ARG:HH21	1.86	0.41
1:S:1422:LEU:HD21	1:S:1433:SER:HB3	2.03	0.41
10:U:32:LEU:HD12	10:U:71:CYS:SG	2.60	0.41
10:U:65:ARG:HA	10:U:68:ILE:HG22	2.01	0.41
11:V:265:LEU:HD12	11:V:265:LEU:HA	1.90	0.41
11:V:443:LEU:HD22	11:V:451:ILE:HG23	2.03	0.41
11:V:1001:PHE:HD2	11:V:1004:LEU:HD22	1.86	0.41
11:V:1041:ASN:OD1	11:V:1042:HIS:N	2.54	0.41
1:A:376:GLN:HG3	1:A:410:TRP:CE3	2.56	0.41
1:A:471:VAL:HG22	1:A:510:TYR:OH	2.21	0.41
2:B:279:LEU:HD23	2:B:303:PHE:CE1	2.55	0.41
2:B:756:ILE:HG23	8:P:866:LEU:CD1	2.51	0.41
4:E:524:ARG:HG2	4:E:525:LYS:N	2.35	0.41
6:G:345:GLN:O	6:G:349:ILE:HG12	2.21	0.41
6:H:63:ALA:O	6:H:67:LEU:HD12	2.19	0.41
7:M:218:LYS:O	7:M:218:LYS:HD3	2.20	0.41
2:O:94:ILE:O	2:O:109:LEU:HD12	2.20	0.41
2:O:323:GLU:O	2:O:324:LYS:CG	2.69	0.41
8:P:384:GLU:O	8:P:385:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:P:809:GLN:O	8:P:813:THR:HG23	2.21	0.41
8:Q:191:PRO:HD2	8:Q:194:LEU:HD22	2.03	0.41
1:S:446:LEU:HB3	1:S:449:ALA:HB3	2.02	0.41
1:S:1128:GLN:HB2	1:S:1173:TRP:CD2	2.54	0.41
10:U:819:ARG:HA	10:U:819:ARG:HD2	1.93	0.41
11:V:242:THR:HG22	11:V:246:LEU:CD1	2.51	0.41
11:V:817:LYS:HA	11:V:820:VAL:HG12	2.02	0.41
2:B:836:ARG:O	2:B:840:LEU:HG	2.21	0.41
5:F:122:ARG:NE	5:F:122:ARG:HA	2.34	0.41
2:O:331:ASP:OD1	2:O:332:ASP:N	2.48	0.41
2:O:762:THR:HA	2:O:765:LYS:HE3	2.03	0.41
8:P:32:GLU:HG3	8:P:33:ALA:H	1.86	0.41
8:P:399:LEU:O	8:P:399:LEU:HD23	2.20	0.41
8:Q:70:LEU:O	8:Q:74:ARG:N	2.54	0.41
8:Q:287:ALA:C	8:Q:288:LEU:HD22	2.40	0.41
1:S:193:LEU:HB3	1:S:241:MET:SD	2.60	0.41
1:S:722:LEU:O	1:S:725:SER:OG	2.26	0.41
1:S:1359:ASP:HA	1:S:1362:LEU:HD12	2.03	0.41
10:U:421:LEU:O	10:U:422:GLY:C	2.59	0.41
10:U:500:LEU:HA	10:U:503:VAL:HG12	2.03	0.41
10:U:619:LEU:HD23	10:U:619:LEU:HA	1.94	0.41
10:U:635:TYR:CE2	10:U:705:ILE:HG23	2.56	0.41
11:V:296:GLU:HG2	11:V:297:VAL:N	2.36	0.41
11:V:423:VAL:HG12	11:V:424:HIS:ND1	2.36	0.41
11:V:477:LEU:HD23	11:V:477:LEU:HA	1.91	0.41
11:V:646:PRO:HA	11:V:649:LEU:HD12	2.03	0.41
1:A:30:VAL:HG11	6:H:372:ALA:CB	2.51	0.41
1:A:236:SER:HA	1:A:239:VAL:HG12	2.03	0.41
1:A:410:TRP:O	1:A:414:LEU:HD23	2.21	0.41
1:A:424:LEU:HD23	1:A:424:LEU:HA	1.93	0.41
1:A:753:MET:SD	1:A:761:VAL:HG21	2.61	0.41
1:A:1173:TRP:O	1:A:1177:LEU:HG	2.21	0.41
1:A:1193:LEU:HD21	1:A:1197:LEU:HB2	2.03	0.41
1:A:1272:HIS:CA	1:A:1281:LEU:HD21	2.50	0.41
1:A:1293:GLU:HA	1:A:1296:GLU:OE1	2.20	0.41
1:A:1325:ASP:OD1	1:A:1326:GLN:NE2	2.54	0.41
2:B:481:ARG:HD3	2:B:632:TYR:O	2.21	0.41
2:B:725:THR:HG22	2:O:585:SER:HB3	2.01	0.41
4:E:408:GLN:OE1	4:E:445:PRO:HD2	2.21	0.41
6:G:31:GLN:O	6:G:39:ARG:NH1	2.49	0.41
6:G:77:PHE:HE2	6:G:95:ASP:OD2	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:483:LEU:HD23	6:G:513:ARG:CG	2.51	0.41
6:G:518:ILE:HD11	6:G:550:THR:HG22	2.02	0.41
6:H:21:ASP:O	6:H:25:ARG:HD3	2.21	0.41
6:H:90:GLU:OE1	6:H:90:GLU:N	2.51	0.41
6:H:524:TRP:CE3	6:H:524:TRP:HA	2.56	0.41
7:L:168:ASP:OD1	7:L:169:PHE:N	2.54	0.41
7:M:29:ILE:HD11	7:M:88:LYS:HE3	2.03	0.41
7:M:101:LEU:HD23	7:M:101:LEU:HA	1.88	0.41
2:O:134:LEU:HD12	2:O:135:ARG:N	2.35	0.41
2:O:146:HIS:CE1	2:O:149:ALA:HB3	2.56	0.41
2:O:657:LYS:HE3	2:O:718:ILE:HG21	2.03	0.41
8:P:136:LEU:HD21	8:P:199:SER:HB2	2.03	0.41
8:Q:253:VAL:HG21	8:Q:258:LEU:HD12	2.03	0.41
8:Q:325:LYS:HB3	8:Q:337:GLU:HG3	2.03	0.41
8:Q:763:ASN:OD1	8:Q:764:VAL:N	2.53	0.41
1:S:287:GLU:OE1	1:S:287:GLU:N	2.53	0.41
1:S:393:VAL:HA	1:S:396:LEU:HD12	2.02	0.41
1:S:722:LEU:HD21	1:S:753:MET:SD	2.61	0.41
1:S:915:THR:HA	1:S:918:GLU:HG2	2.03	0.41
1:S:1351:GLU:O	1:S:1414:SER:OG	2.31	0.41
1:S:1392:PRO:O	1:S:1395:LEU:HB3	2.21	0.41
10:U:75:LEU:HD12	10:U:81:LEU:HD11	2.03	0.41
10:U:236:PHE:CE2	10:U:240:LEU:HD11	2.56	0.41
10:U:606:TYR:HB3	10:U:670:CYS:SG	2.60	0.41
10:U:757:ASN:ND2	10:U:770:ASP:HB2	2.35	0.41
10:U:761:SER:OG	10:U:762:SER:N	2.53	0.41
11:V:108:ASP:OD1	11:V:109:SER:N	2.54	0.41
11:V:110:PHE:HZ	11:V:176:ILE:HD13	1.86	0.41
11:V:387:ILE:HG12	11:V:431:MET:HE3	2.03	0.41
11:V:791:ASN:HB3	11:V:926:ARG:HG2	2.02	0.41
11:V:1128:PHE:HE2	11:V:1181:GLN:HB3	1.85	0.41
11:V:1303:GLU:O	11:V:1307:LYS:HG2	2.21	0.41
1:A:473:LEU:O	1:A:476:PHE:HB3	2.21	0.41
1:A:662:ALA:O	1:A:665:THR:HG23	2.21	0.41
1:A:1176:SER:HA	1:S:964:LEU:HD21	2.03	0.41
1:A:1354:LEU:O	1:A:1358:VAL:HG13	2.21	0.41
2:B:84:ASP:OD1	2:B:85:PHE:N	2.54	0.41
2:B:324:LYS:O	2:B:325:LEU:HB2	2.21	0.41
3:C:146:TYR:HD1	3:C:146:TYR:HA	1.81	0.41
4:E:373:LEU:HD23	4:E:373:LEU:HA	1.92	0.41
6:G:541:VAL:HG21	6:G:554:LEU:CD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:237:ASN:O	7:L:251:CYS:HA	2.21	0.41
7:M:167:VAL:HG21	7:M:169:PHE:CE2	2.55	0.41
2:O:522:LYS:C	2:O:523:CYS:SG	2.99	0.41
1:S:45:GLU:HA	1:S:48:VAL:HG12	2.03	0.41
1:S:362:LEU:HD23	1:S:365:MET:SD	2.61	0.41
10:U:910:GLU:OE2	10:U:914:LYS:HE3	2.21	0.41
1:A:310:VAL:O	8:P:831:ARG:NE	2.54	0.40
1:A:1017:ILE:HD13	1:A:1017:ILE:HA	1.94	0.40
2:B:279:LEU:HD23	2:B:303:PHE:HZ	1.84	0.40
2:B:690:GLU:H	2:B:690:GLU:CD	2.23	0.40
2:B:780:HIS:NE2	2:B:831:SER:HB3	2.36	0.40
3:C:328:LYS:HE3	3:C:329:ALA:HB2	2.03	0.40
5:F:238:VAL:HG12	5:F:270:LEU:HD21	2.03	0.40
6:G:38:ARG:O	6:G:42:LEU:HD13	2.21	0.40
6:G:178:LEU:HD12	6:G:178:LEU:HA	1.91	0.40
6:G:388:PRO:O	6:G:501:GLN:NE2	2.54	0.40
7:M:134:SER:OG	7:M:135:THR:N	2.54	0.40
7:M:147:GLU:OE1	7:M:147:GLU:N	2.54	0.40
2:O:106:GLU:O	2:O:107:TYR:HB2	2.20	0.40
8:P:367:CYS:HA	8:P:392:PRO:HA	2.04	0.40
8:Q:86:TYR:CE2	8:Q:123:CYS:HB2	2.57	0.40
8:Q:232:ASP:OD1	8:Q:233:ALA:N	2.49	0.40
8:Q:582:LEU:O	8:Q:582:LEU:HG	2.21	0.40
1:S:156:LEU:HD23	1:S:190:ILE:HD13	2.03	0.40
1:S:1071:ARG:O	1:S:1075:LEU:HG	2.21	0.40
10:U:270:THR:HA	10:U:273:LEU:HD12	2.01	0.40
10:U:611:ASP:OD1	10:U:614:ARG:NH1	2.44	0.40
11:V:668:SER:HA	11:V:761:PHE:HZ	1.86	0.40
11:V:927:GLU:OE2	11:V:1001:PHE:HA	2.21	0.40
11:V:1289:PRO:HA	11:V:1352:ARG:HH12	1.85	0.40
1:A:363:PHE:HB3	1:A:400:PHE:CZ	2.56	0.40
1:A:931:ASP:O	1:A:935:LEU:HG	2.20	0.40
1:A:1392:PRO:HA	1:A:1395:LEU:CG	2.50	0.40
2:B:774:SER:HB2	8:P:834:HIS:ND1	2.36	0.40
3:C:364:TRP:CH2	3:C:538:ILE:HG13	2.54	0.40
4:E:351:LEU:HG	4:E:352:SER:O	2.21	0.40
4:E:356:SER:HB3	7:M:73:ARG:HD2	2.02	0.40
6:H:137:SER:OG	6:H:190:GLU:HG3	2.21	0.40
6:H:395:GLU:HA	6:H:398:LEU:HD12	2.02	0.40
7:M:226:ARG:HD3	7:M:226:ARG:HA	1.97	0.40
8:P:67:LEU:HD22	8:P:76:LEU:HD21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Q:588:GLU:HB3	8:Q:591:GLY:HA3	2.03	0.40
10:U:15:ASP:OD1	10:U:16:LYS:HG2	2.21	0.40
10:U:66:ARG:HH12	10:U:70:THR:HG23	1.87	0.40
10:U:102:GLY:HA3	10:U:144:LEU:HD11	2.02	0.40
10:U:365:LEU:HB3	10:U:369:LYS:NZ	2.36	0.40
10:U:968:ASN:HA	10:U:971:SER:HG	1.86	0.40
11:V:211:ILE:O	11:V:214:SER:OG	2.29	0.40
11:V:281:ILE:O	11:V:284:PHE:HB3	2.20	0.40
11:V:568:PHE:CD2	11:V:851:THR:HG21	2.54	0.40
11:V:794:ARG:NE	11:V:926:ARG:O	2.42	0.40
11:V:1031:HIS:CE1	11:V:1062:TYR:HB2	2.57	0.40
1:A:1048:LEU:HD23	1:A:1048:LEU:HA	1.95	0.40
2:B:73:HIS:NE2	2:B:101:LYS:HE2	2.36	0.40
2:B:90:ASN:C	2:B:91:LEU:HG	2.41	0.40
3:C:415:ALA:HB1	3:C:450:LEU:HD21	2.03	0.40
4:E:141:ARG:HB3	4:E:147:GLY:HA3	2.03	0.40
6:G:251:ALA:O	6:G:254:SER:OG	2.26	0.40
6:G:389:PRO:HA	6:G:501:GLN:HE22	1.86	0.40
6:G:457:LEU:HB2	6:G:479:CYS:SG	2.62	0.40
6:G:473:ILE:HG21	6:G:524:TRP:CH2	2.56	0.40
6:G:565:ASP:OD1	6:G:566:GLU:HG3	2.21	0.40
7:M:207:ILE:HD11	7:M:280:VAL:HG21	2.02	0.40
8:P:77:TYR:HE1	8:P:87:CYS:SG	2.43	0.40
8:P:250:LEU:HD21	8:P:276:HIS:HB3	2.04	0.40
1:S:555:ILE:HD11	1:S:599:SER:HB2	2.03	0.40
1:S:822:LEU:HD21	1:S:824:CYS:SG	2.62	0.40
10:U:290:VAL:O	10:U:294:LYS:N	2.55	0.40
10:U:369:LYS:O	10:U:372:VAL:HG12	2.22	0.40
11:V:792:TRP:NE1	11:V:796:ILE:HD11	2.35	0.40
11:V:1010:GLN:NE2	11:V:1075:TRP:HE1	2.19	0.40
11:V:1056:HIS:O	11:V:1059:SER:OG	2.36	0.40
1:A:29:ARG:HD3	1:A:29:ARG:N	2.37	0.40
1:A:214:LEU:HD13	1:A:273:MET:SD	2.61	0.40
1:A:1134:PHE:CZ	1:A:1138:LEU:HD21	2.56	0.40
1:A:1334:ALA:O	1:A:1338:LEU:HD23	2.22	0.40
2:B:356:SER:OG	2:B:356:SER:O	2.39	0.40
2:B:822:LYS:HA	2:B:825:GLN:HG3	2.02	0.40
3:C:62:GLU:OE1	3:C:63:ARG:NH2	2.54	0.40
6:H:237:SER:O	6:H:237:SER:OG	2.37	0.40
7:L:125:LYS:HE2	7:L:187:TYR:CE2	2.56	0.40
2:O:105:PHE:O	2:O:126:LEU:N	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:170:ILE:HG23	2:O:170:ILE:O	2.22	0.40
2:O:237:VAL:CG2	2:O:258:ALA:HB1	2.51	0.40
2:O:520:LEU:CD2	8:P:518:GLN:HB3	2.49	0.40
2:O:749:SER:O	2:O:755:LEU:HD11	2.22	0.40
8:P:27:ARG:C	8:P:400:ASN:ND2	2.71	0.40
8:P:221:GLU:HG3	8:P:308:HIS:HB3	2.03	0.40
8:P:572:LEU:HA	8:P:572:LEU:HD12	1.85	0.40
8:Q:30:CYS:HB3	8:Q:35:VAL:HG12	2.02	0.40
8:Q:192:HIS:HD2	8:Q:193:PHE:CE2	2.39	0.40
1:S:92:SER:HA	1:S:154:TYR:CE2	2.55	0.40
1:S:1243:ARG:HE	1:S:1286:HIS:CE1	2.39	0.40
1:S:1319:LEU:HA	1:S:1322:VAL:HG12	2.03	0.40
1:S:1336:TYR:HD2	1:S:1364:LEU:HD13	1.87	0.40
10:U:605:LEU:HD13	10:U:605:LEU:HA	1.95	0.40
10:U:718:LEU:HD23	10:U:725:LYS:HE2	2.04	0.40
10:U:895:SER:OG	10:U:896:GLY:N	2.55	0.40
10:U:1089:LEU:O	10:U:1093:GLU:HG3	2.21	0.40
11:V:222:SER:HG	11:V:223:GLN:H	1.69	0.40
11:V:794:ARG:HA	11:V:797:VAL:HG22	2.04	0.40
11:V:1359:LEU:HA	11:V:1362:LYS:HE2	2.03	0.40
1:A:1139:LEU:HD23	1:A:1143:LEU:HD12	2.03	0.40
1:A:1155:ILE:HD13	1:A:1158:LYS:NZ	2.36	0.40
1:A:1255:GLU:HG3	1:A:1259:PHE:CE2	2.57	0.40
3:C:72:ALA:O	3:C:76:TRP:HE3	2.04	0.40
3:C:127:PHE:HA	5:F:147:ARG:NH2	2.37	0.40
3:C:287:HIS:ND1	3:C:289:ALA:HB3	2.36	0.40
4:E:37:PRO:C	4:E:39:GLY:H	2.24	0.40
4:E:140:LEU:HA	4:E:140:LEU:HD12	1.82	0.40
4:E:313:LEU:HA	4:E:313:LEU:HD12	1.89	0.40
4:E:396:TYR:HB3	4:E:397:PRO:HD3	2.03	0.40
5:F:260:LEU:O	5:F:264:THR:HG23	2.21	0.40
6:G:414:LEU:HD21	6:G:462:ALA:HB3	2.02	0.40
6:H:342:THR:O	6:H:345:GLN:N	2.55	0.40
2:O:509:LEU:O	2:O:595:CYS:HA	2.22	0.40
8:Q:673:ARG:HG2	8:Q:677:ALA:CB	2.52	0.40
1:S:428:VAL:HG22	1:S:476:PHE:CZ	2.56	0.40
10:U:1060:ILE:HG13	10:U:1061:ASP:N	2.35	0.40
11:V:765:LEU:HD22	11:V:786:ILE:HG13	2.03	0.40
11:V:1037:LEU:O	11:V:1041:ASN:ND2	2.55	0.40
11:V:1089:SER:O	11:V:1093:VAL:HG23	2.21	0.40
11:V:1234:PHE:O	11:V:1238:MET:HB2	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [\(i\)](#)

### 5.3.1 Protein backbone [\(i\)](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	1160/1477 (78%)	1066 (92%)	86 (7%)	8 (1%)	22 62
1	S	1224/1477 (83%)	1126 (92%)	98 (8%)	0	100 100
2	B	685/884 (78%)	595 (87%)	75 (11%)	15 (2%)	6 38
2	O	685/884 (78%)	592 (86%)	84 (12%)	9 (1%)	12 48
3	C	546/583 (94%)	496 (91%)	48 (9%)	2 (0%)	34 72
4	E	411/555 (74%)	400 (97%)	9 (2%)	2 (0%)	29 68
5	F	336/399 (84%)	316 (94%)	20 (6%)	0	100 100
6	G	567/641 (88%)	514 (91%)	52 (9%)	1 (0%)	47 81
6	H	532/641 (83%)	491 (92%)	40 (8%)	1 (0%)	47 81
7	L	368/394 (93%)	334 (91%)	33 (9%)	1 (0%)	41 76
7	M	368/394 (93%)	333 (90%)	32 (9%)	3 (1%)	19 60
8	P	726/906 (80%)	626 (86%)	80 (11%)	20 (3%)	5 33
8	Q	732/906 (81%)	644 (88%)	74 (10%)	14 (2%)	8 41
9	W	21/39 (54%)	13 (62%)	8 (38%)	0	100 100
10	U	1150/1328 (87%)	1056 (92%)	88 (8%)	6 (0%)	29 68
11	V	1131/1451 (78%)	1060 (94%)	65 (6%)	6 (0%)	29 68
All	All	10642/12959 (82%)	9662 (91%)	892 (8%)	88 (1%)	24 60

All (88) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	754	CYS
2	B	148	LYS
2	B	324	LYS

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Mol	Chain	Res	Type
4	E	353	PRO
2	O	147	VAL
2	O	324	LYS
2	O	637	PRO
8	P	449	GLU
8	P	572	LEU
8	P	721	ASP
8	Q	49	GLN
8	Q	720	LYS
8	Q	782	ILE
1	A	288	GLU
1	A	947	SER
1	A	972	GLY
2	B	133	GLY
2	B	147	VAL
2	B	316	PHE
2	B	325	LEU
3	C	23	ASP
4	E	77	PRO
7	M	108	PRO
2	O	83	SER
2	O	638	LYS
8	P	32	GLU
8	P	720	LYS
8	P	750	ALA
8	P	781	PRO
8	P	782	ILE
8	Q	572	LEU
8	Q	649	MET
8	Q	781	PRO
10	U	296	GLY
10	U	356	HIS
2	B	138	ASN
2	B	313	LYS
2	B	354	LEU
3	C	279	SER
7	L	216	PRO
7	M	105	PRO
7	M	216	PRO
8	P	384	GLU
8	P	860	CYS
8	Q	518	GLN

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Mol	Chain	Res	Type
8	Q	538	ASP
8	Q	586	PRO
11	V	307	LEU
11	V	414	GLU
11	V	753	ASP
11	V	767	PRO
11	V	777	LYS
1	A	287	GLU
1	A	1221	ASN
2	B	78	CYS
6	H	239	LEU
2	O	217	LEU
8	P	63	GLN
8	P	387	PRO
8	P	727	PRO
8	P	875	HIS
8	Q	557	ASP
10	U	120	SER
10	U	978	ASN
2	B	140	PRO
6	G	192	ASP
2	O	84	ASP
8	P	557	ASP
8	Q	674	ASP
8	Q	721	ASP
1	A	755	GLY
8	P	148	ALA
8	P	166	PRO
8	P	595	PRO
8	Q	595	PRO
10	U	376	ASP
2	B	273	PRO
2	B	637	PRO
8	P	822	ALA
10	U	27	GLY
1	A	1222	PRO
2	B	712	PRO
2	O	140	PRO
2	O	636	PHE
8	P	161	GLY
11	V	379	VAL
8	Q	573	GLY

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Mol	Chain	Res	Type
2	B	610	PRO

### 5.3.2 Protein sidechains [\(i\)](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1034/1282 (81%)	1028 (99%)	6 (1%)	86 92
1	S	1092/1282 (85%)	1090 (100%)	2 (0%)	93 96
2	B	644/810 (80%)	640 (99%)	4 (1%)	86 92
2	O	641/810 (79%)	635 (99%)	6 (1%)	78 88
3	C	480/507 (95%)	477 (99%)	3 (1%)	86 92
4	E	358/467 (77%)	354 (99%)	4 (1%)	73 85
5	F	288/336 (86%)	287 (100%)	1 (0%)	92 95
6	G	483/538 (90%)	480 (99%)	3 (1%)	86 92
6	H	454/538 (84%)	451 (99%)	3 (1%)	84 90
7	L	334/354 (94%)	331 (99%)	3 (1%)	78 88
7	M	334/354 (94%)	333 (100%)	1 (0%)	92 95
8	P	627/749 (84%)	614 (98%)	13 (2%)	53 72
8	Q	630/749 (84%)	627 (100%)	3 (0%)	88 93
9	W	22/22 (100%)	21 (96%)	1 (4%)	27 54
10	U	1066/1204 (88%)	1052 (99%)	14 (1%)	69 82
11	V	1065/1324 (80%)	1049 (98%)	16 (2%)	65 80
All	All	9552/11326 (84%)	9469 (99%)	83 (1%)	79 88

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ARG
1	A	30	VAL
1	A	714	ARG

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Mol	Chain	Res	Type
1	A	845	LEU
1	A	1032	GLN
1	A	1308	LEU
2	B	353	CYS
2	B	401	CYS
2	B	521	LEU
2	B	523	CYS
3	C	66	THR
3	C	146	TYR
3	C	343	TYR
4	E	90	LEU
4	E	98	LEU
4	E	295	LEU
4	E	524	ARG
5	F	101	ARG
6	G	23	LEU
6	G	89	THR
6	G	594	GLU
6	H	12	CYS
6	H	373	LEU
6	H	538	LEU
7	L	30	SER
7	L	46	LEU
7	L	152	LEU
7	M	297	ILE
2	O	9	SER
2	O	477	LYS
2	O	505	THR
2	O	611	LYS
2	O	640	LYS
2	O	779	LYS
8	P	16	CYS
8	P	199	SER
8	P	201	SER
8	P	219	THR
8	P	315	PHE
8	P	390	LEU
8	P	399	LEU
8	P	402	CYS
8	P	567	ILE
8	P	607	ARG
8	P	643	SER

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Mol	Chain	Res	Type
8	P	655	PHE
8	P	839	THR
8	Q	222	ASP
8	Q	252	CYS
8	Q	339	ARG
1	S	32	ARG
1	S	460	ARG
9	W	79	THR
10	U	11	GLU
10	U	306	SER
10	U	307	PRO
10	U	369	LYS
10	U	435	MET
10	U	483	GLU
10	U	495	THR
10	U	615	ARG
10	U	750	CYS
10	U	753	LEU
10	U	898	LYS
10	U	905	SER
10	U	976	ASP
10	U	1199	LYS
11	V	91	LYS
11	V	135	LEU
11	V	185	ARG
11	V	302	ARG
11	V	310	CYS
11	V	342	CYS
11	V	371	THR
11	V	378	LYS
11	V	436	LEU
11	V	562	GLN
11	V	729	CYS
11	V	774	MET
11	V	1015	CYS
11	V	1130	CYS
11	V	1228	ARG
11	V	1364	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (163) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	123	GLN
1	A	158	HIS
1	A	200	HIS
1	A	248	GLN
1	A	292	HIS
1	A	343	GLN
1	A	352	HIS
1	A	417	GLN
1	A	423	GLN
1	A	669	GLN
1	A	767	GLN
1	A	771	HIS
1	A	913	HIS
1	A	1057	GLN
1	A	1118	ASN
1	A	1128	GLN
1	A	1190	GLN
1	A	1272	HIS
1	A	1355	HIS
1	A	1437	GLN
2	B	73	HIS
2	B	99	ASN
2	B	306	ASN
2	B	431	GLN
2	B	525	ASN
2	B	656	HIS
2	B	670	ASN
2	B	679	HIS
2	B	846	GLN
3	C	107	GLN
3	C	212	GLN
3	C	441	GLN
3	C	468	GLN
3	C	493	ASN
4	E	123	GLN
4	E	163	GLN
4	E	359	ASN
4	E	455	GLN
5	F	7	HIS
5	F	43	HIS
5	F	63	HIS
5	F	144	HIS

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Mol	Chain	Res	Type
5	F	149	ASN
5	F	211	GLN
5	F	244	ASN
5	F	283	GLN
6	G	20	ASN
6	G	31	GLN
6	G	94	GLN
6	G	140	HIS
6	G	201	GLN
6	G	501	GLN
6	G	510	GLN
6	G	511	GLN
6	G	547	ASN
6	G	553	HIS
6	H	20	ASN
6	H	31	GLN
6	H	224	ASN
6	H	456	HIS
6	H	461	GLN
7	L	37	HIS
7	L	99	GLN
7	L	189	GLN
7	L	272	HIS
7	L	331	GLN
7	M	37	HIS
7	M	76	HIS
7	M	148	HIS
7	M	331	GLN
7	M	335	GLN
7	M	350	GLN
2	O	10	ASN
2	O	71	ASN
2	O	73	HIS
2	O	90	ASN
2	O	116	ASN
2	O	270	ASN
2	O	350	ASN
2	O	608	ASN
2	O	656	HIS
2	O	679	HIS
2	O	724	GLN
2	O	729	GLN

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Mol	Chain	Res	Type
2	O	733	ASN
2	O	746	ASN
8	P	66	HIS
8	P	192	HIS
8	P	249	GLN
8	P	277	HIS
8	P	317	HIS
8	P	382	GLN
8	P	734	GLN
8	P	815	GLN
8	P	845	GLN
8	Q	92	HIS
8	Q	192	HIS
8	Q	360	HIS
8	Q	400	ASN
8	Q	531	ASN
8	Q	589	ASN
8	Q	734	GLN
8	Q	815	GLN
8	Q	845	GLN
1	S	123	GLN
1	S	186	HIS
1	S	227	HIS
1	S	374	HIS
1	S	492	HIS
1	S	563	ASN
1	S	582	HIS
1	S	716	HIS
1	S	913	HIS
1	S	986	ASN
1	S	1128	GLN
1	S	1437	GLN
10	U	110	ASN
10	U	172	GLN
10	U	266	HIS
10	U	298	GLN
10	U	304	ASN
10	U	320	GLN
10	U	325	GLN
10	U	345	GLN
10	U	373	HIS
10	U	417	HIS

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Mol	Chain	Res	Type
10	U	433	HIS
10	U	465	ASN
10	U	580	ASN
10	U	597	GLN
10	U	621	ASN
10	U	673	HIS
10	U	836	ASN
10	U	929	GLN
10	U	973	GLN
10	U	978	ASN
10	U	1071	HIS
10	U	1091	GLN
10	U	1137	GLN
10	U	1193	ASN
10	U	1204	HIS
10	U	1278	HIS
11	V	66	ASN
11	V	72	GLN
11	V	76	GLN
11	V	81	GLN
11	V	86	HIS
11	V	146	GLN
11	V	198	GLN
11	V	377	HIS
11	V	471	GLN
11	V	545	ASN
11	V	562	GLN
11	V	746	ASN
11	V	748	ASN
11	V	937	HIS
11	V	1010	GLN
11	V	1026	HIS
11	V	1092	HIS
11	V	1258	GLN
11	V	1280	ASN
11	V	1355	GLN

### 5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [\(i\)](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	W	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	W	9:UNK	C	73:GLU	N	36.69
1	W	95:TRP	C	101:UNK	N	7.00

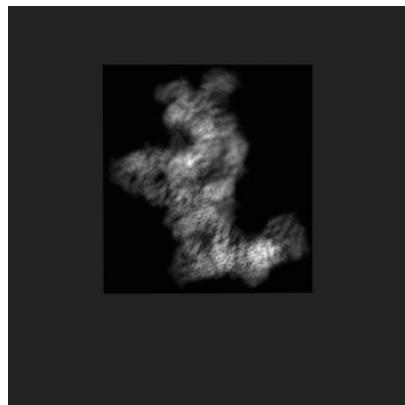
## 6 Map visualisation i

This section contains visualisations of the EMDB entry EMD-23086. These allow visual inspection of the internal detail of the map and identification of artifacts.

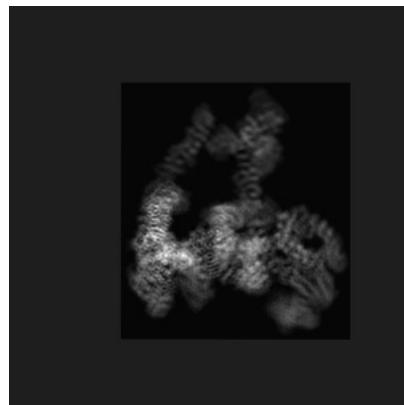
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections i

#### 6.1.1 Primary map



X



Y



Z

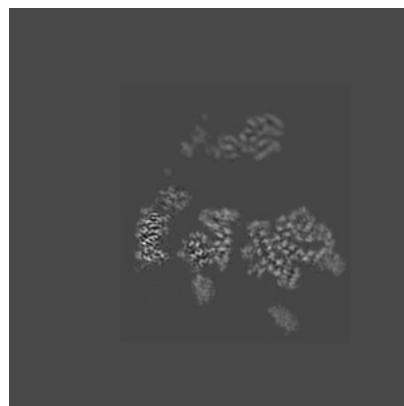
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices i

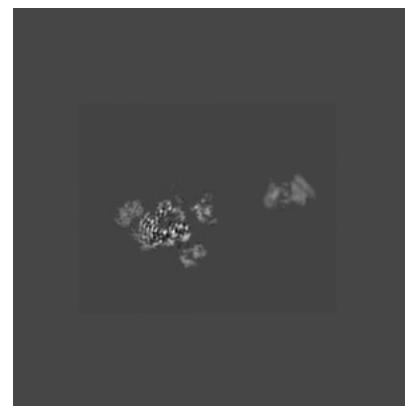
#### 6.2.1 Primary map



X Index: 224



Y Index: 224



Z Index: 224

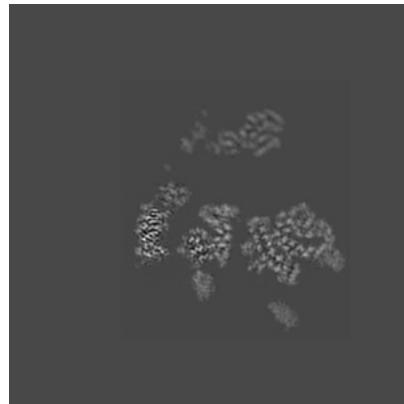
The images above show central slices of the map in three orthogonal directions.

### 6.3 Largest variance slices [\(i\)](#)

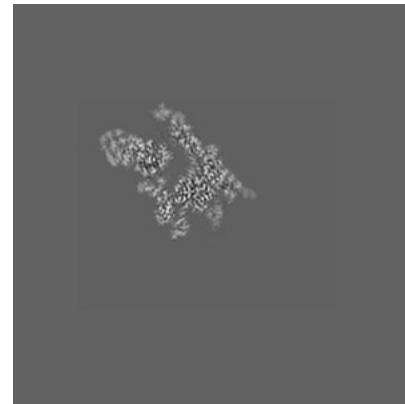
#### 6.3.1 Primary map



X Index: 168



Y Index: 224

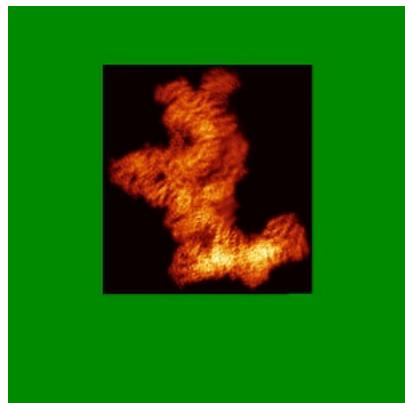


Z Index: 168

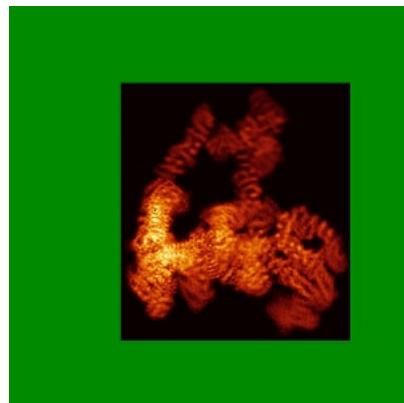
The images above show the largest variance slices of the map in three orthogonal directions.

### 6.4 Orthogonal standard-deviation projections (False-color) [\(i\)](#)

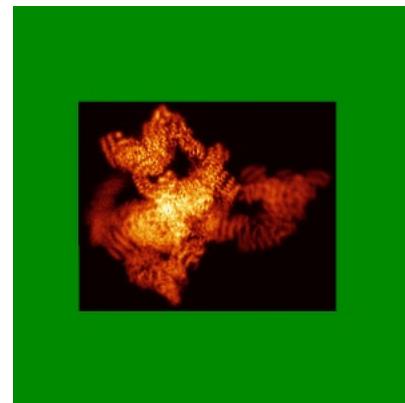
#### 6.4.1 Primary map



X



Y

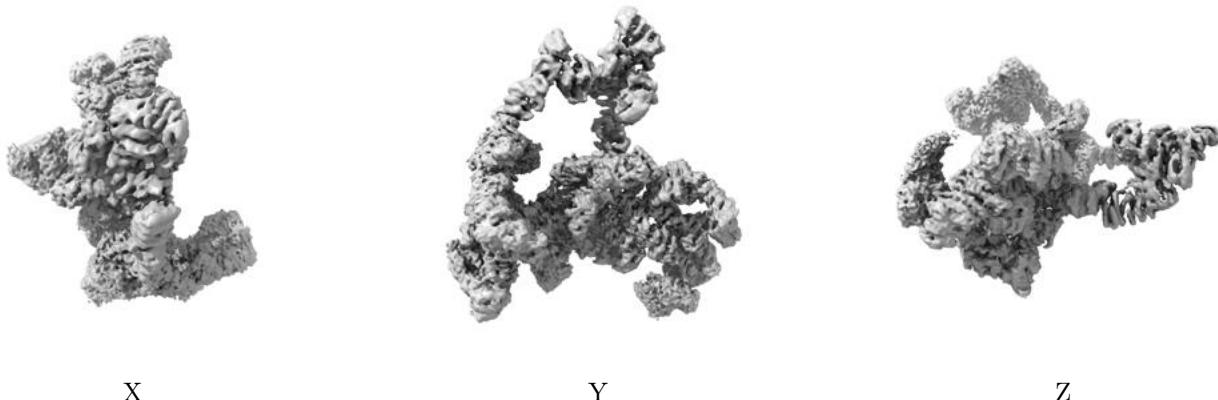


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [\(i\)](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

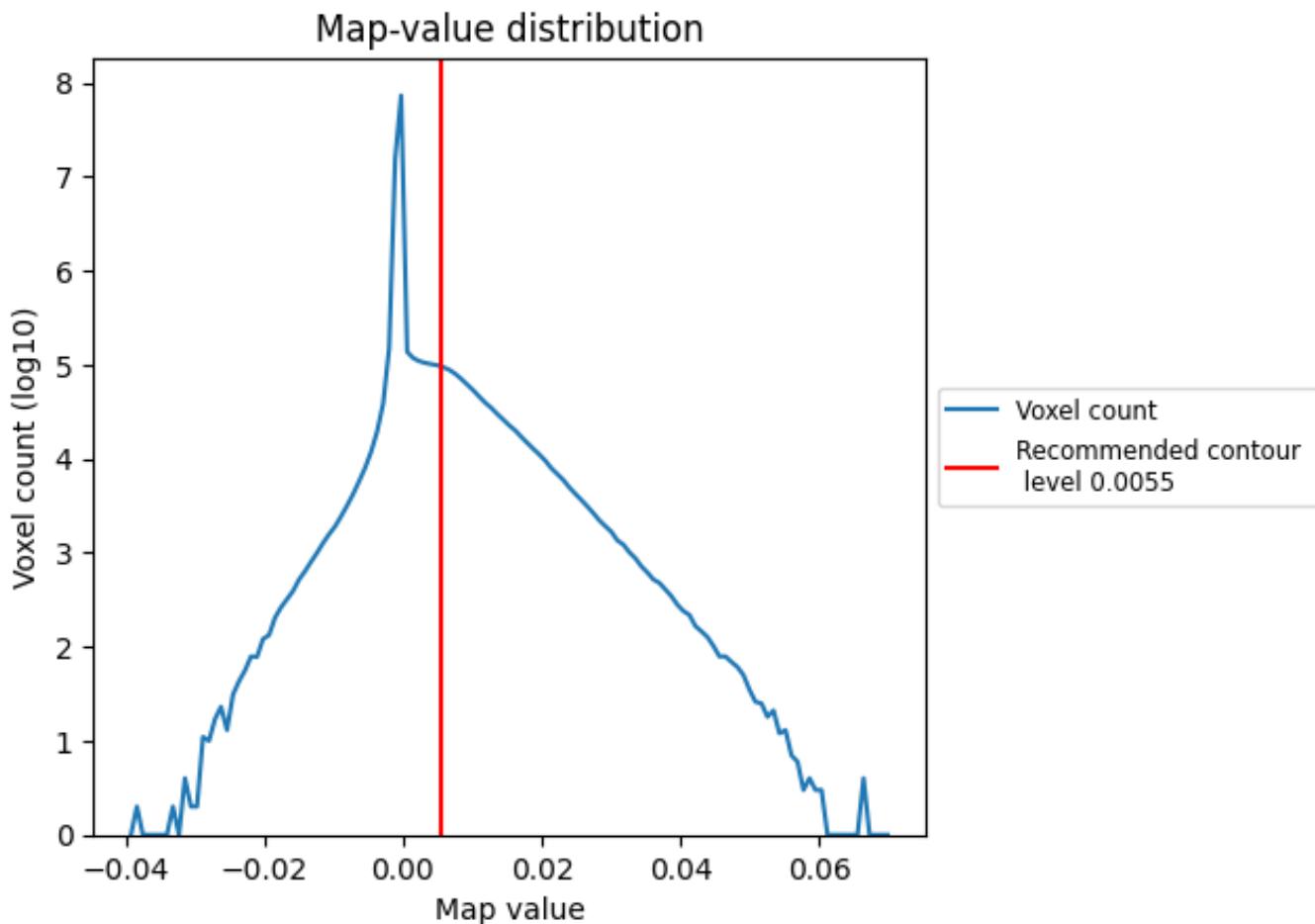
## 6.6 Mask visualisation [\(i\)](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis (i)

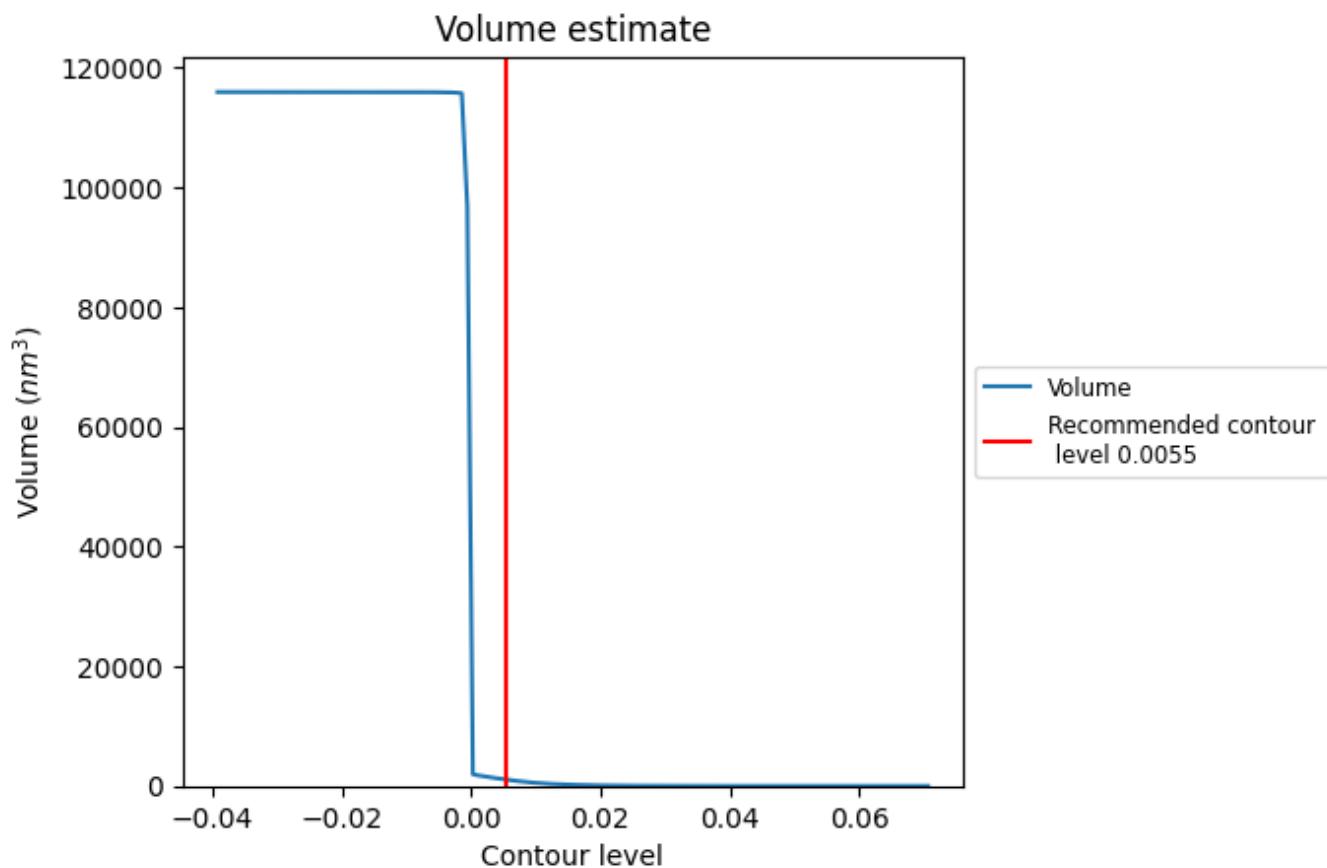
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

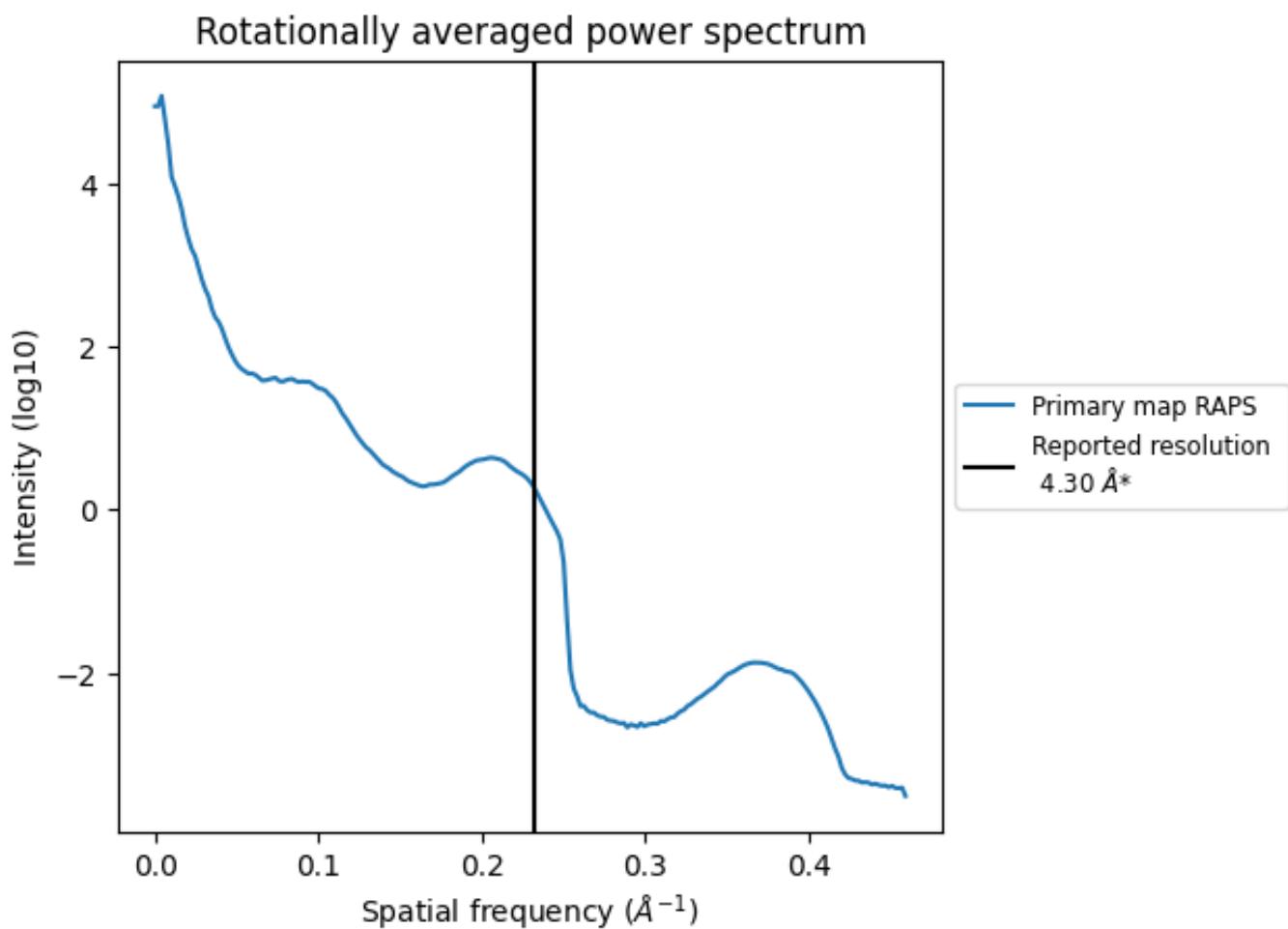
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1056 nm<sup>3</sup>; this corresponds to an approximate mass of 954 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of  $0.233 \text{ \AA}^{-1}$

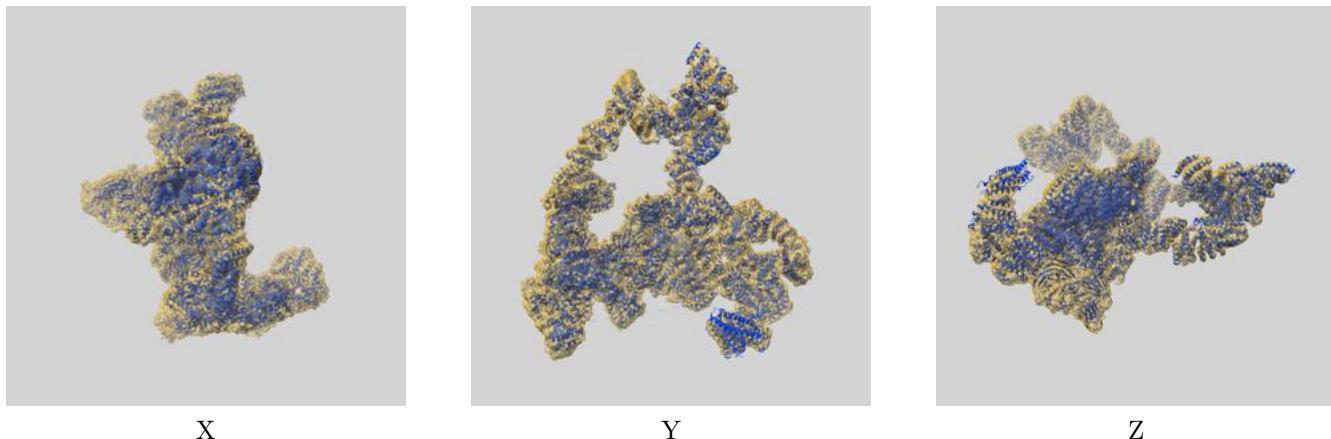
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit i

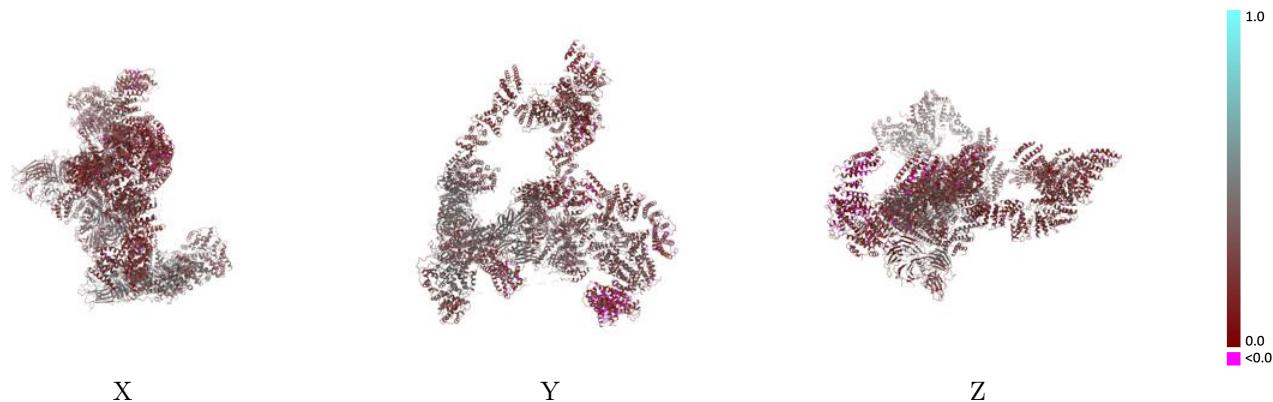
This section contains information regarding the fit between EMDB map EMD-23086 and PDB model 7KZQ. Per-residue inclusion information can be found in section 3 on page 14.

### 9.1 Map-model overlay i



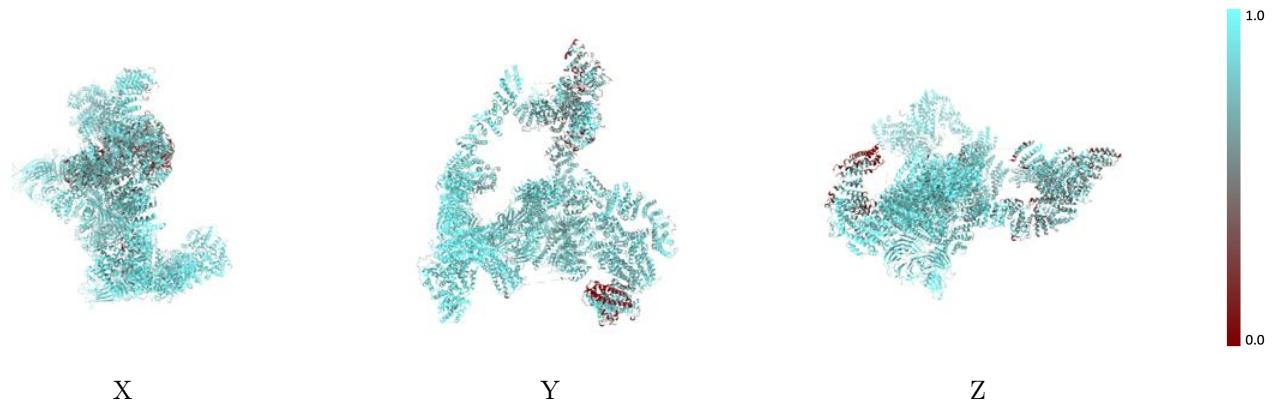
The images above show the 3D surface view of the map at the recommended contour level 0.0055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [\(i\)](#)



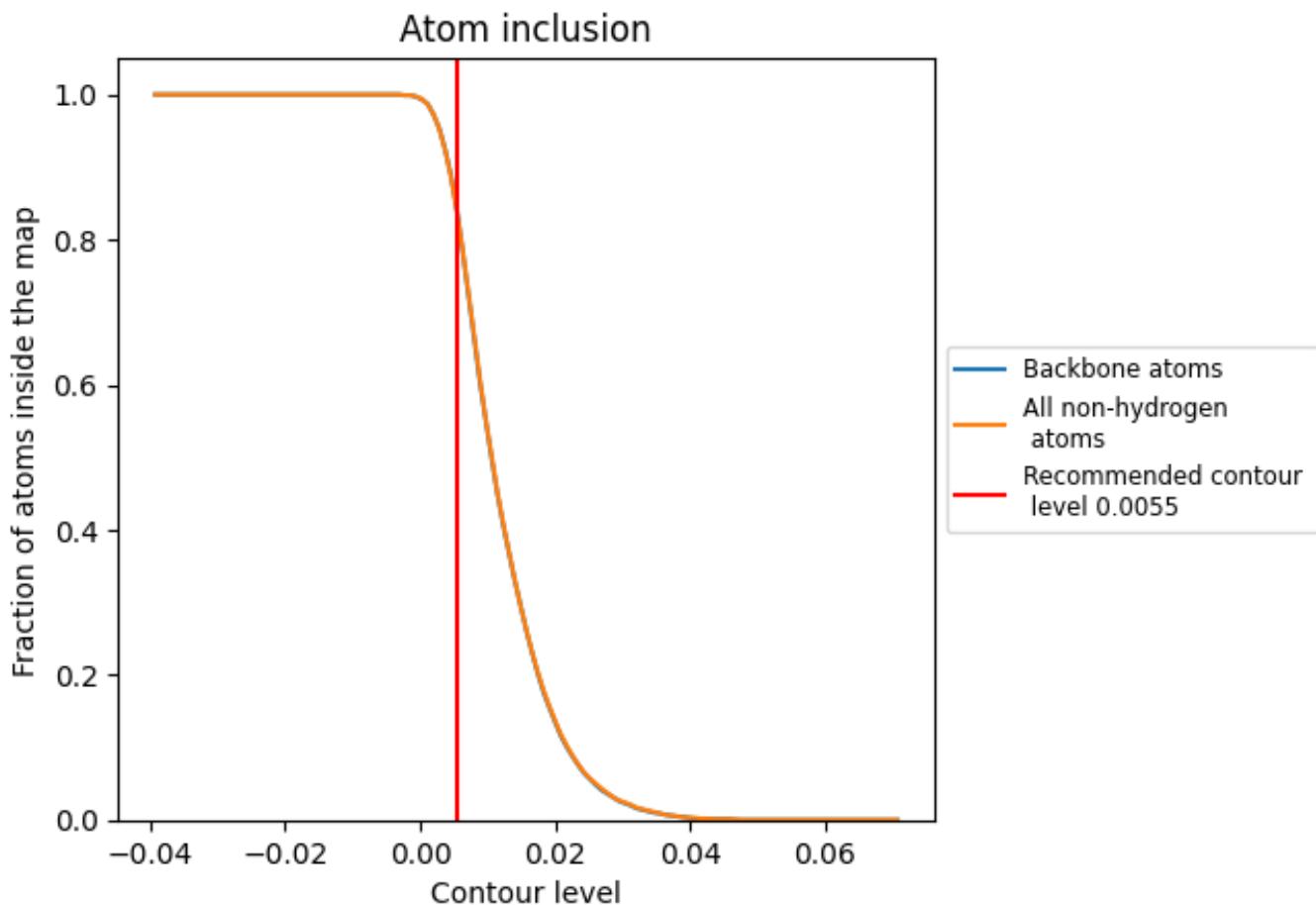
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [\(i\)](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0055).

## 9.4 Atom inclusion [\(i\)](#)



At the recommended contour level, 84% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8360	0.2980
A	0.7390	0.2360
B	0.9210	0.3940
C	0.9510	0.3710
E	0.8730	0.3550
F	0.9480	0.3640
G	0.8810	0.3380
H	0.8480	0.2740
L	0.9370	0.3810
M	0.9010	0.3080
O	0.9100	0.3130
P	0.9400	0.4100
Q	0.9050	0.2980
S	0.7160	0.2390
U	0.8690	0.2570
V	0.7190	0.2130
W	0.7360	0.2920

